

DR WPI: 1999-045276/04.
DR P-PSDB: AAM85475.

Composition containing antagonist of growth factor GP88 - useful for
treating cancer and viral diseases and also for diagnosing disease
from altered GP88 expression

XX PS Disclosure: Fig 9A; 86pp; English.

CC This human cDNA sequence includes a coding region for GP88 (see
CC AAM85474), an 88 kDa glycoprotein autocrine growth factor and
CC epithelial/granulin precursor that is expressed in a tightly
CC regulated manner in normal cells, is overexpressed and unregulated
CC in highly tumorigenic cells derived from normal cells, and which
CC acts as a stringently required growth stimulator for the
CC tumorigenic cells. Inhibition of GP88 expression or action in the
CC properties of the overproducing cells. Antagonists to GP88 are
CC used to treat diseases associated with increased expression of
CC GP88, particularly cancer but also viral infections. Fragments of
CC GP88 are used to raise specific antibodies (used as antagonists,
CC as diagnostic reagents and for delivering toxins or other
CC compounds to GP88-expressing cells) and to screen for antibodies.
CC Antisense oligonucleotides can also be used as antagonists.
CC Methods are provided for diagnosing disease, or determining
CC susceptibility to disease, resulting from altered GP88 activity.
CC XX

Sequence 2095 BP; 364 A; 681 C; 625 G; 425 T; 0 other;

Query Match 99.9%; Score 2093.4; DB 20; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCAGGACAGCATGTGACCTGTGAGCTGGTGGCTTAACAGCAGGCTGTGCT 60
DB 1 CGCAGGACAGCATGTGACCTGTGAGCTGGTGGCTTAACAGCAGGCTGTGCT 60
QY 61 GGAACGGGCGCCAGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 GGAACGGGCGCCAGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 GCCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GCCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GTGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GTGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GTCTAGGAGACTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GTCTAGGAGACTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GGTAAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 GGTAAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TGCCTGGAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 TGCCTGGAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 CGCTGATACACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
DB 541 CGCTGATACACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

QY 601 AACAGGACAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AACAGGACAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 CACACAGTGGGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 900
DB 841 CACACAGTGGGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 900
QY 901 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GACACATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 GACACATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 CAGGGGCGCCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 CAGGGGCGCCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CCACAAGCTTGAAGAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CCACAAGCTTGAAGAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 ACCCTGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 ACCCTGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TGCCTGGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 TGCCTGGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TGCCTGGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TGCCTGGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 AAGGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740

Db	1681	CAGTGGTCCTGCTGGCTTCCGCTGCGACCGACGGGGTACCAAGTGTGGCGAGGAG	1740
Qy	1741	GGCCCGCGCTGGGAGCGCCCTTTGAGAGGACCCAGCCTTGAGACAGCTGCTGTAGGGACA	1800
Db	1741	GGCCCGCGCTGGGAGCGCCCTTTGAGAGGACCCAGCCTTGAGACAGCTGCTGTAGGGACA	1800
Qy	1801	GTAAGTGAAGACTCTGAGCCCTGCGGACCCCACTCGGAGGGTGCCTCTGCTGAGGCTC	1860
Db	1801	GTAAGTGAAGACTCTGAGCCCTGCGGACCCCACTCGGAGGGTGCCTCTGCTGAGGCTC	1860
Qy	1861	CCTAGCACCCTCCCTTACCAAAATTCCTCCCTGGACCCCAATTCGAGCTCCCATCACCAT	1920
Db	1861	CCTAGCACCCTCCCTTACCAAAATTCCTCCCTGGACCCCAATTCGAGCTCCCATCACCAT	1920
Qy	1921	GGGAGGTGGGGCTCAATTAAGGGCCCTCCCTGTAAGAGGGGGTTGAGGCAAAAGCC	1980
Db	1921	GGGAGGTGGGGCTCAATTAAGGGCCCTCCCTGTAAGAGGGGGTTGAGGCAAAAGCC	1980
Qy	1981	ATTACAAAGCTGCCATCCCTCCCGTTTCAAGTGGACCCCTGAGCCAGTCTTTCCCTA	2040
Db	1981	ATTACAAAGCTGCCATCCCTCCCGTTTCAAGTGGACCCCTGAGCCAGTCTTTCCCTA	2040
Qy	2041	TCCACAGGGGTGTTGTGTGTGGGTGTCTTCAATAAAGTTGTACATTCTT	2095
Db	2041	TCCACAGGGGTGTTGTGTGTGGGTGTCTTCAATAAAGTTGTACATTCTT	2095
RESULT 2			
AA056794			
ID	AA056794 standard; DNA; 2124 BP.		
XX	AC	AA056794;	
XX	DT	22-APR-1994 (first entry)	
XX	DE	Granulin coding sequence.	
XX	KM	Granulin; keratinocytes; wound healing; inhibition; peptide;	
XX	KW	granulocytes; leucocytes; ss.	
XX	OS	Homo sapiens.	
XX	FH	Key	location/Qualifiers
XX	FT	misc_difference 1379..1381	
XX	FT	/*tag= a	
XX	FT	misc_difference 1640..1642	
XX	FT	/*tag= b	
XX	FT	/transl_except= CAG encodes Glycine.	
XX	PM	W09315195-A.	
XX	PD	05-AUG-1993.	
XX	PF	28-FEB-1992; 92MO-CA00089.	
XX	PR	03-FEB-1992; 92US-0829233.	
XX	PA	(SOLO/) SOLOMON S.	
XX	PI	Solomon S;	
XX	DR	WPI; 1993-320328/40.	
XX	DR	P-PSDB; AAR48673.	
XX	PT	New cystine rich granulin peptide(s) from leucocyte(s) - are	
XX	PT	keratinocyte inhibitors useful topically for wound healing	
XX	PS	Disclosure; Figure 4c; 53bp; English.	
XX	CC	The granulin inhibits keratinocytes and is useful in formulations	
XX	CC	for promoting the healing of wounds.	

XX	Sequence	2124 BP: 383 A: 685 C: 630 G: 426 T: 0 other:	
50	Query Match	99.9%; Score 2093.4; DB 14; Length 2124;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2094; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 CCCAGGACGACCATGTGTGACCCCTGTGTGACCTGGGTGGCTTTAAACAGCAGGCTGTGGCT	60	
DB	14 CCCAGGACGACCATGTGTGACCCCTGTGTGACCTGGGTGGCTTTAAACAGCAGGCTGTGGCT	73	
QY	61 GGAAGCGGGTGGCCAGATGTGATTCCTGCTGGTGGCTGGCTGGTGGCTGGTGGCTGGTGG	120	
DB	74 GGAAGCGGGTGGCCAGATGTGATTCCTGCTGGTGGCTGGCTGGTGGCTGGTGGCTGGTGG	133	
QY	121 GCCAGCTACAGCTGTGCTGCCGTCCTCTTGGACAATGTGCCCAACAACACTGACAGAGCAT	180	
DB	134 GCCAGCTACAGCTGTGCTGCCGTCCTCTTGGACAATGTGCCCAACAACACTGACAGAGCAT	193	
QY	181 CTGGGTGGCCCCCTGCCAGGTTGATGCCCCACTGCTGCGGGCACTCTGTGACTTTTACC	240	
DB	194 CTGGGTGGCCCCCTGCCAGGTTGATGCCCCACTGCTGCGGGCACTCTGTGACTTTTACC	253	
QY	241 GTCCTAGGAGCTTCCAGTTGCTGCCCTTCCAGAGGCGGTGGCAATGGGGATGGCCCAT	300	
DB	254 GTCCTAGGAGCTTCCAGTTGCTGCCCTTCCAGAGGCGGTGGCAATGGGGATGGCCCAT	313	
QY	301 CACTGCTGCCACGAGGAGCTTCCACTGTGACAGAGGAGGAGCTGCTTCCAAAGATCA	360	
DB	314 CACTGCTGCCACGAGGAGCTTCCACTGTGACAGAGGAGGAGCTGCTTCCAAAGATCA	373	
QY	361 GGTAAACACTCCGTGGGTGCATCCAGTGCCTGATATGTGAGTATGCCCGGACTTC	420	
DB	374 GGTAAACACTCCGTGGGTGCATCCAGTGCCTGATATGTGAGTATGCCCGGACTTC	433	
QY	421 TCCAGTGTGTGATATGATGATGGCTCTGTGGGGTGTGCCCATATGCCCAAGGCTTCC	480	
DB	434 TCCAGTGTGTGATATGATGATGGCTCTGTGGGGTGTGCCCATATGCCCAAGGCTTCC	493	
QY	481 TGCCTGTGAAGACAGGGTGCATGCTGTCCGACAGGAGCTTGTGACACTGGTTACACC	540	
DB	494 TGCCTGTGAAGACAGGGTGCATGCTGTCCGACAGGAGCTTGTGACACTGGTTACACC	553	
QY	541 CGCTGCATCACACCAACGAGGACCCACCCCTGTGGCAAGAAGCTCCCTCCAGAGACT	600	
DB	554 CGCTGCATCACACCAACGAGGACCCACCCCTGTGGCAAGAAGCTCCCTCCAGAGACT	613	
QY	601 AACAGGACAGTGGCTTGTCCAGCTGGTGCATATGTGTCCGAGACGACAGGTGCCGTCC	660	
DB	614 AACAGGACAGTGGCTTGTCCAGCTGGTGCATATGTGTCCGAGACGACAGGTGCCGTCC	673	
QY	661 GATGGTTTACACTGCTGTGATGCTGCCAGTGGGAATATGGGTGGTGGCCAAATGGCCAAC	720	
DB	674 GATGGTTTACACTGCTGTGATGCTGCCAGTGGGAATATGGGTGGTGGCCAAATGGCCAAC	733	
QY	721 GCCACCTGCTGCTCCGATACCTGCATGCTGCCCAAGACACTGTGTGTGACCTGATC	780	
DB	734 GCCACCTGCTGCTCCGATACCTGCATGCTGCCCAAGACACTGTGTGTGACCTGATC	793	
QY	781 CAGAGTAACTGCTCTCCAGAGAAACGTTACACGAGACTCTCTCACTAAGCTGCTGCG	840	
DB	794 CAGAGTAACTGCTCTCCAGAGAAACGTTACACGAGACTCTCTCACTAAGCTGCTGCG	853	
QY	841 CACACAGTGGGAGATGTGAATGTGATGATGAGAGGTGAGTGTGCCAGATGGCATATACCTCC	900	
DB	854 CACACAGTGGGAGATGTGAATGTGATGATGAGAGGTGAGTGTGCCAGATGGCATATACCTCC	913	
QY	901 TGGCGTTTACACTCGGGGGCTGGGGGCTGCTCCCTTTTACCAGAGCTTGTGCTGTGAG	960	
DB	914 TGGCGTTTACACTCGGGGGCTGGGGGCTGCTCCCTTTTACCAGAGCTTGTGCTGTGAG	973	
QY	961 GACCAATTAACACTGCTGTCCCGGGGGTTTACGTGTGACACGCAAGAGGTAACCTGTGA	1020	

QY 301 CACTGCTGCCACGGGGCTTCCATGTCAGTGCAGACGGGGCATCTCTTCCAAAGATCA 360
 DB 388 CACTGCTGCCACGGGGCTTCCATGTCAGTGCAGACGGGGCATCTCTTCCAAAGATCA 447
 QY 361 GGTAACTCCGTGGGTCATCCAGTGCCTGATAGTCAATTTGAATGCCGGGACTTC 420
 DB 448 GGTAACTCCGTGGGTCATCCAGTGCCTGATAGTCAATTTGAATGCCGGGACTTC 507
 QY 421 TCACGTCTGTATGATGTCATGCTCTTGGGGTGTGTCCTCATGCCAGGCTTC 480
 DB 508 TCACGTCTGTATGATGTCATGCTCTTGGGGTGTGTCCTCATGCCAGGCTTC 567
 QY 481 TGTGTGAAGACAGGGTGCATGCTGTCCGACGGTGCCTTCTGCACTGGTTACACC 540
 DB 568 TGTGTGAAGACAGGGTGCATGCTGTCCGACGGTGCCTTCTGCACTGGTTACACC 627
 QY 541 CGCTGCATACACCCACGGGGACCCACCCCTGCGAAAGAAAGTCTCCCTCCAGAGACT 600
 DB 628 CGCTGCATACACCCACGGGGACCCACCCCTGCGAAAGAAAGTCTCCCTCCAGAGACT 687
 QY 601 AACAGGAGTGGCTTGTCCAGTGGTGCATGTCGAGACAGGTCCTCCGGTCCCT 660
 DB 688 AACAGGAGTGGCTTGTCCAGTGGTGCATGTCGAGACAGGTCCTCCGGTCCCT 747
 QY 661 GATGTTCTACCTGCTGTGAGCTGCGACAGTGGAAATATGCTGCTGCCAAATGCCAAC 720
 DB 748 GATGTTCTACCTGCTGTGAGCTGCGACAGTGGAAATATGCTGCTGCCAAATGCCAAC 807
 QY 721 GCCACCTGCTGTCGATACCTGCATGCTGTCGCCCAAGACACTGTGTACCTGATC 780
 DB 808 GCCACCTGCTGTCGATACCTGCATGCTGTCGCCCAAGACACTGTGTACCTGATC 867
 QY 781 CAGAGTAGTGCCTTCCAAAGAGAACCTACACGACCTCTCACTAAGTGGCTGCG 840
 DB 868 CAGAGTAGTGCCTTCCAAAGAGAACCTACACGACCTCTCACTAAGTGGCTGCG 927
 QY 841 CACACAGTGGCGATGTAATGTACATGAGGTGAGCTGCCAGATGGCTATACCTGC 900
 DB 928 CACACAGTGGCGATGTAATGTACATGAGGTGAGCTGCCAGATGGCTATACCTGC 987
 QY 901 TGGCGTTCACAGTGGGGGCTTGGGGGCTGTCCTTTTACCAGGCTGTGTGCTGTAG 960
 DB 988 TGGCGTTCACAGTGGGGGCTTGGGGGCTGTCCTTTTACCAGGCTGTGTGCTGTAG 1047
 QY 961 GACCACATACACTGCTGTCCGCGGGGTTTACGTGTGACACGACAGAGGTTACTGTGA 1020
 DB 1048 GACCACATACACTGCTGTCCGCGGGGTTTACGTGTGACACGACAGAGGTTACTGTGA 1107
 QY 1021 CAGGGGCCCAACAGAGTCCCTGATGAGAAAGGCCCACTACCTGACCTGCCAGAC 1080
 DB 1108 CAGGGGCCCAACAGAGTCCCTGATGAGAAAGGCCCACTACCTGACCTGCCAGAC 1167
 QY 1081 CCACAAGCTTGAAGAGAGATGTCCCTGTGATTAATGTACAGAGCTGTCCCTCCGAT 1140
 DB 1168 CCACAAGCTTGAAGAGAGATGTCCCTGTGATTAATGTACAGAGCTGTCCCTCCGAT 1227
 QY 1141 ACCTGCTGCCAACTGCTGTGGGAGTGGGCTGCTGTCCAAATCCAGAGGCTGTCTCC 1200
 DB 1228 ACCTGCTGCCAACTGCTGTGGGAGTGGGCTGCTGTCCAAATCCAGAGGCTGTCTCC 1287
 QY 1201 TGTCTGGACACACAGCACTGCTGCCCCCAGCGATACAGTGTGTAGCTGAGGGGAGTGT 1260
 DB 1288 TGTCTGGACACACAGCACTGCTGCCCCCAGCGATACAGTGTGTAGCTGAGGGGAGTGT 1347
 QY 1261 CAGCGAGAGAGAGATGTGGCTGAGTGGAGAGATGTCCCTGCCCGCGCTTCCTTA 1320
 DB 1348 CAGCGAGAGAGAGATGTGGCTGAGTGGAGAGATGTCCCTGCCCGCGCTTCCTTA 1407
 QY 1321 TCCCACTCCAGAGATGAGTGTGTGACCAAGCACACAGCTGCCGCTGGGCGGAACCTGC 1380.
 DB 1408 TCCCACTCCAGAGATGAGTGTGTGACCAAGCACACAGCTGCCGCTGGGCGGAACCTGC 1467

QY 1381 TGCCTGAGCCAGGGTGGGAGCTGGGCTGCTGCTGCAGTGTGCCCATCTGTGTGCTGCAG 1440
 DB 1468 TGCCTGAGCCAGGGTGGGAGCTGGGCTGCTGCTGCAGTGTGCCCATCTGTGTGCTGCAG 1527
 QY 1441 GATCGCACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 DB 1528 GATCGCACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1587
 QY 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 1588 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1647
 QY 1561 AAGGAGTGTGAGTGGGAGGAGACACTTCTGCATGATTAACAGACCTGTGCGAGAC 1620
 DB 1648 AAGGAGTGTGAGTGGGAGGAGACACTTCTGCATGATTAACAGACCTGTGCGAGAC 1707
 QY 1621 AACCCAGAGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1708 AACCCAGAGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1767
 QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 DB 1768 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1827
 QY 1741 GCCCGCGCTGGGAGCCGCTTTGAGGAGCCAGCCTTGAGACAGCTGCTGTGAGGAGA 1800
 DB 1828 GCCCGCGCTGGGAGCCGCTTTGAGGAGCCAGCCTTGAGACAGCTGCTGTGAGGAGA 1887
 QY 1801 GTACTAAAGCTGTGAGGCTTGGGAGCCCACTCGGAGGGTCCCTGTGCTGAGGCTTC 1860
 DB 1888 GTACTAAAGCTGTGAGGCTTGGGAGCCCACTCGGAGGGTCCCTGTGCTGAGGCTTC 1947
 QY 1861 CCTAGCAGCTCCGCTTAACCAATTCCTCTGAGACCCCAATTCGAGCTCCCATACCAT 1920
 DB 1948 CCTAGCAGCTCCGCTTAACCAATTCCTCTGAGACCCCAATTCGAGCTCCCATACCAT 2007
 QY 1921 GGGAGGTGGGCTCAATTAAGGCTTCCCTGTCAGAGAGGGGTTGAGGCAAAAGCC 1980
 DB 2008 GGGAGGTGGGCTCAATTAAGGCTTCCCTGTCAGAGAGGGGTTGAGGCAAAAGCC 2067
 QY 1981 ATTACAGCTGCCATCCCTCCGCTTTCAGTGTGAGACCTGTGGCCAGGTCTTTCCCTA 2040
 DB 2068 ATTACAGCTGCCATCCCTCCGCTTTCAGTGTGAGACCTGTGGCCAGGTCTTTCCCTA 2127
 QY 2041 TCCACAGGGGT 2095
 DB 2128 TCCACAGGGGT 2182

RESULT 4
 AAD32850
 ID AAD32850 standard; cDNA; 2155 BP.
 XX
 AC AAD32850;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human granulin/epithelin precursor (GP88) cDNA.
 XX
 KW Human; granulin precursor; GP88; cytosolic; tumorigenicity; tamoxifen;
 KW antineoplastic; antioestrogen therapy; skin cancer; gene; ss.
 OS Homo sapiens.
 XX
 FH
 FT Key
 FT misc_feature
 FT 1..374
 FT /tag= a
 FT /note= "This region is cloned in the antisense
 FT orientation in pCDNA3 mammalian expression vector"
 FT 13..1794
 FT /tag= b
 FT /product= "Human GP88 protein"
 FT /transl_except= (pos:829..831, aa:Tyr)


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Db 1501 AAGGAGGTCCTGCTCCAGCCCTCCACCTTCCTGGCCCGGAGCCCTACGCGGTG 1560
Oy 1561 AAGGAGGTCCTGCTCCAGCCCTCCACCTTCCTGGCCCGGAGCCCTACGCGGTG 1620
Db 1561 AAGGAGGTCCTGCTCCAGCCCTCCACCTTCCTGGCCCGGAGCCCTACGCGGTG 1620
Oy 1621 AACCGACAGGGGCTGGGCTGCTGCTCCCTACGCGCGGCTGCTGCTGCTGCTG 1680
Db 1621 AACCGACAGGGGCTGGGCTGCTGCTCCCTACGCGCGGCTGCTGCTGCTGCTG 1680
Oy 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Oy 1741 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCCTTGAAGAGCTGCTGAGGAG 1800
Db 1741 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCCTTGAAGAGCTGCTGAGGAG 1800
Oy 1801 ----- 1800
Db 1801 GTACTGAGACTCTGACGCCCTCGGAGCCCACTCGAGGGTGGCTGCTGCTGAG 1860
Oy 1801 GTACTGAGACTCTGACGCCCTCGGAGCCCACTCGAGGGTGGCTGCTGCTGAG 1860
Db 1861 GTACTGAGACTCTGACGCCCTCGGAGCCCACTCGAGGGTGGCTGCTGCTGAG 1920
Oy 1861 CTTAGCAGCTCCCTTAACCAATTCCTGCTGAGCCCACTGCTGAGCTCCCA 1920
Db 1921 CTTAGCAGCTCCCTTAACCAATTCCTGCTGAGCCCACTGCTGAGCTCCCA 1980
Oy 1921 GGGAGGTGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAGGGGGTGAAGCA 1980
Db 1981 GGGAGGTGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAGGGGGTGAAGCA 2040
Oy 1981 ATTAAAGCTGCTATCCCTCCCTGCTGAGGAGCCCTGCTGAGGCTGCTGCT 2040
Db 2041 ATTAAAGCTGCTATCCCTCCCTGCTGAGGAGCCCTGCTGAGGCTGCTGCT 2100
Oy 2041 TCCAGAGGGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2095
Db 2101 TCCAGAGGGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2155

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RESULT 5
ABK64817
ID ABR64817 standard; DNA; 2152 BP.
XX ABR64817;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human benign prostatic hyperplasia gene #712.
XX
XX Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200212440-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 07-AUG-2001; 2001WO-US24708.
XX
XX PR 07-AUG-2000; 2000US-223323P.
XX
XX PR 05-JUN-2001; 2001US-0873319.
XX
XX PA (GENE-) GENE LOGIC INC.
XX
XX PA (NISB) JAPAN TOBACCO INC.
XX
XX Munger WE, Kulikarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
XX WPI: 2002-257476/30.

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XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells
XX
PS Disclosure; Page 395-396; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the gene expression
CC agent, and comparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABR64106 ABR64660 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 2152 BP; 394 A; 691 C; 639 G; 428 T; 0 other;

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Query Match 96.1%; Score 2014; DB 24; Length 2152;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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Oy 1 CGCAGGAGACATATGAGACCTGCTGAGCTGGTGGCTTAAACAGCAGGCGTGGT 60
Db 29 CGCAGGAGACATATGAGACCTGCTGAGCTGGTGGCTTAAACAGCAGGCGTGGT 88
Oy 61 GGAACGCGGTGCCAGATGTCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 89 GGAACGCGGTGCCAGATGTCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Oy 121 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 149 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 208
Oy 181 CTGGGTGGCCCTGCCAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 209 CTGGGTGGCCCTGCCAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 268
Oy 241 GTCTCAGGAGCTTCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 269 GTCTCAGGAGCTTCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328
Oy 301 CACTGCTGCCAGGCGGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 360
Db 329 CACTGCTGCCAGGCGGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 388
Oy 361 GGTAAACATCCGTGGGTGCATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 420
Db 389 GGTAAACATCCGTGGGTGCATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 448
Oy 421 TCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 449 TCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
Oy 481 TGCTGTGAAGACAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 509 TGCTGTGAAGACAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568

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QY 541 CGCTGCATCACACCCAGGCGACCCCGGCGAAGAAAGCTCTCTGCCCAGAGACT 600
 Db 569 CGCTGCATCACACCCAGGCGACCCCGGCGAAGAAAGCTCTCTGCCCAGAGACT 628
 QY 601 AACAGGCGAGTGGCTTGTGCACTGCTGATGTCGCGAGAGAGAGAGAGAGAG 660
 Db 629 AACAGGCGAGTGGCTTGTGCACTGCTGATGTCGCGAGAGAGAGAGAGAGAG 688
 QY 661 GATGCTTACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 Db 689 GATGCTTACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
 QY 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 749 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
 QY 781 CAGAGTAGTGTCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 809 CAGAGTAGTGTCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
 QY 841 CACACAGTGGGCGATGTGAATGTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 869 CACACAGTGGGCGATGTGAATGTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
 QY 901 TGCCGCTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 929 TGCCGCTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 988
 QY 961 GACCACTATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 Db 989 GACCACTATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1048
 QY 1021 CAGGCGCGCCAGCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1049 CAGGCGCGCCAGCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1108
 QY 1081 CCACAGCCTTGAAGAGAGATGTCCCTGTGAATGTGACAGAGAGAGAGAGAGAG 1140
 Db 1109 CCACAGCCTTGAAGAGAGATGTCCCTGTGAATGTGACAGAGAGAGAGAGAGAG 1168
 QY 1141 ACCTGCTGCACTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 Db 1169 ACCTGCTGCACTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1228
 QY 1201 TCTCTGAGCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1229 TCTCTGAGCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1288
 QY 1261 CAGCAGAGAGAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Db 1289 CAGCAGAGAGAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348
 QY 1321 TCCACCCAGAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Db 1349 TCCACCCAGAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1408
 QY 1381 TGCCGAGCCAGAGAGTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1409 TGCCGAGCCAGAGAGTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1468
 QY 1441 GATGCGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 Db 1469 GATGCGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1528
 QY 1501 AAGGAAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1529 AAGGAAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1588
 QY 1561 AAGGAGCTGAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 Db 1589 AAGGAGCTGAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1648
 QY 1621 AACCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680

Db 1649 AACCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1708
 QY 1681 CACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 Db 1709 CACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1768
 QY 1741 GCGCGCGCTGCGAGCGCGCGCTTGAAGGAGCCAGCGCTTGAAGAGAGAGAGAGAGAG 1800
 Db 1769 GCGCGCGCTGCGAGCGCGCGCTTGAAGGAGCCAGCGCTTGAAGAGAGAGAGAGAGAG 1828
 QY 1801 GTACTGAAGACTGTGAGCGCTGCGAGCGCGCTTGAAGGAGAGAGAGAGAGAGAGAGAG 1860
 Db 1829 GTACTGAAGACTGTGAGCGCTGCGAGCGCGCTTGAAGGAGAGAGAGAGAGAGAGAGAG 1888
 QY 1861 CCTAGACCTCCCGCTAACCAAAATTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 Db 1889 CCTAGACCTCCCGCTAACCAAAATTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1948
 QY 1921 GCGAGGTGGGCGCTGAATCTAGGCGCTTCCCTGTCAGAGAGAGAGAGAGAGAGAGAGAG 1979
 Db 1949 GCGAGGTGGGCGCTGAATCTAGGCGCTTCCCTGTCAGAGAGAGAGAGAGAGAGAGAGAG 2007
 QY 1980 CATTTCAAGCTGCGCAATCCCTCCGCTTTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2039
 Db 2008 CATTTCAAGCTGCGCAATCCCTCCGCTTTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2067
 QY 2040 ATCCACAGGAGGT 2061
 Db 2068 ATCCACAGGAGGT 2089

RESULT 6
 ABR83501
 ID ABR83501 standard; cDNA; 2178 BP.
 AC ABR83501;
 AC ABR83501;
 DT 14-AUG-2002 (first entry)
 DE Human cDNA differentially expressed in granulocytic cells #72.
 XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; AIDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; peridontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US30821.
 XX
 PR 03-OCT-2000; 2000US-237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weltsman SM, Yamaga S, Vockley J;
 DR WPI; 2002-435328/46.
 XX
 DR
 XX
 PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity
 XX
 PS Claim 1; SEQ ID No 72; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) Gs by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GCA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC inflammation injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 2178 BP; 401 A; 697 C; 646 G; 434 T; 0 other;

XX Query Match 96.1%; Score 2014; DB 24; Length 2178;

XX Best Local Similarity 99.2%; Pred. No. 0;

XX Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 1 CGCAGCGACACCATGATGACCTGGTGGTGGCTTTACAGCAGGGCTGGTGGT 60
DB 51 CGCAGCGACACCATGATGACCTGGTGGTGGCTTTACAGCAGGGCTGGTGGT 110
QY 61 GGAACGGGGTCCCAAGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 111 GGAACGGGGTCCCAAGATGATGATGATGATGATGATGATGATGATGATGAT 170
QY 121 GCGAGCTACAGCTGCTCCGCTCCCTCTGGACAATGAGCCACACACTAGCAGGAT 180
DB 171 GCGAGCTACAGCTGCTCCGCTCCCTCTGGACAATGAGCCACACACTAGCAGGAT 230
QY 181 CTGGGGTGGCCCTGCGAGGTTGATGACCACTGCTGCGGCACTCTGATCTTTACC 240
DB 231 CTGGGGTGGCCCTGCGAGGTTGATGACCACTGCTGCGGCACTCTGATCTTTACC 290
QY 241 GTCTCAGAGGACTTCAATGTGCTGCCCTTCCCAAGAGCCGTGGCATGGGGATGGCCAT 300
DB 291 GTCTCAGAGGACTTCAATGTGCTGCCCTTCCCAAGAGCCGTGGCATGGGGATGGCCAT 350
QY 301 CACTGCTGCCAGGGGGCTTCACTGAGTGCAGAGGGGGCATGCTGCTTCAAGATCA 360
DB 351 CACTGCTGCCAGGGGGCTTCACTGAGTGCAGAGGGGGCATGCTGCTTCAAGATCA 410
QY 361 GGTAAACAGTCCGTTGGTGCATCAGTGCCTGATAGTCAATGCAATGCGGACTTC 420
DB 411 GGTAAACAGTCCGTTGGTGCATCAGTGCCTGATAGTCAATGCAATGCGGACTTC 470
QY 421 TCCACGTGCTGTATTATGATGATGATGATGATGATGATGATGATGATGATGAT 480

DB 471 TCCACGTGCTGTATTATGATGATGATGATGATGATGATGATGATGATGATGAT 530
QY 481 TCCCTGAAGAGAGGTGACGCTGTCGCGACAGCGGTGCTTGTGACCTGTTACANCC 540
DB 531 TCCCTGAAGAGAGGTGACGCTGTCGCGACAGCGGTGCTTGTGACCTGTTACANCC 590
QY 541 CGCTCATCACACCACAGGGGACCCACCCCTGGCAAGAAAGACTCCCTGCCAGAGACT 600
DB 591 CGCTCATCACACCACAGGGGACCCACCCCTGGCAAGAAAGACTCCCTGCCAGAGACT 650
QY 601 AACAGGGCAGTGGCTTGTCCAGCTCGGTGATGTGTCCGAGACAGAGTCCCGTGCCT 660
DB 651 AACAGGGCAGTGGCTTGTCCAGCTCGGTGATGTGTCCGAGACAGAGTCCCGTGCCT 710
QY 661 GATGTTTACCTGCTGAGAGTGGAGTGGGAGTATGGTGTGCCCATGGCCACAC 720
DB 711 GATGTTTACCTGCTGAGAGTGGAGTGGGAGTATGGTGTGCCCATGGCCACAC 770
QY 721 GCCACCTGCTGCTCCGATCACCTGCTGCTGCTCCCAAGACACTGTGTGACCTGATC 780
DB 771 GCCACCTGCTGCTCCGATCACCTGCTGCTGCTCCCAAGACACTGTGTGACCTGATC 830
QY 781 CAGATTAAGTCTCTTCCAGAGAGAACCTTACACAGGACTTCTCACTAAGCTGCTGCG 840
DB 831 CAGATTAAGTCTCTTCCAGAGAGAACCTTACACAGGACTTCTCACTAAGCTGCTGCG 890
QY 841 CACACAGTGGGGAGTGAATGTGACATGAGAGTGGAGTGGCCAGATGGCATACCTCC 900
DB 891 CACACAGTGGGGAGTGAATGTGACATGAGAGTGGAGTGGCCAGATGGCATACCTCC 950
QY 901 TGCCCTTACAGTCCGGGGCTGCGGCTGCTGCTCCCTTTTACCAGAGTGTGTGCTGTGAG 960
DB 951 TGCCCTTACAGTCCGGGGCTGCGGCTGCTGCTCCCTTTTACCAGAGTGTGTGCTGTGAG 1010
QY 961 GACCATATATCATGCTGTGTCCCGGGGTTTACGTGTGACACCCAGAGAGGTACCTGTGA 1020
DB 1011 GACCATATATCATGCTGTGTCCCGGGGTTTACGTGTGACACCCAGAGAGGTACCTGTGA 1070
QY 1021 CAGGGGCCCCACAGAGTGGCTGATGAGAGAGGCCCCAGCTACCTGAGCTGCGACAGC 1080
DB 1071 CAGGGGCCCCACAGAGTGGCTGATGAGAGAGGCCCCAGCTACCTGAGCTGCGACAGC 1130
QY 1081 CCACAAGCTTTGAAGAGAGATGCTCCCTGTGTATATGTGACGAGCTGTCCCTCCGAT 1140
DB 1131 CCACAAGCTTTGAAGAGAGATGCTCCCTGTGTATATGTGACGAGCTGTCCCTCCGAT 1190
QY 1141 ACCTGCTGCAACTCAGCTGTGGGAGTGGGCTGTGTCCAAATCCCAAGAGCTGTCTGC 1200
DB 1191 ACCTGCTGCAACTCAGCTGTGGGAGTGGGCTGTGTCCAAATCCCAAGAGCTGTCTGC 1250
QY 1201 TGCTGGAGACACACAGCTGCTGCCCCAGAGATACAGTGTGTAGTGAAGGGGAGTGT 1260
DB 1251 TGCTGGAGACACACAGCTGCTGCCCCAGAGCTTACAGTGTGTAGTGAAGGGGAGTGT 1310
QY 1261 CAGCGAGGAAGGAGATGCTGTGACTGAGAAAGATGCTGCCCGCGCGGTTCTCTTA 1320
DB 1311 CAGCGAGGAAGGAGATGCTGTGACTGAGAAAGATGCTGCCCGCGCGGCTTCTCTTA 1370
QY 1321 TCCCAACCCAGAGACATGGGCTGTGACACAGCACACAGCTGCCCCGGTGGCGGAACCTGC 1380
DB 1371 TCCCAACCCAGAGACATGGGCTGTGACACAGCACACAGCTGCCCCGGTGGCGGAACCTGC 1430
QY 1381 TGCCCGAGCGAAGGGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1431 TGCCCGAGCGAAGGGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1490
QY 1441 GATGCTCAGCACTGCTGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1491 GATGCTCAGCACTGCTGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1550
QY 1501 AAGGAAGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

Db 1551 AAGGAGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1610
 Qy 1561 AAGGAGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1620
 Db 1611 AAGGAGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1670
 Qy 1621 AAGGAGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1680
 Db 1671 AAGGAGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1730
 Qy 1681 CACTGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1740
 Db 1731 CACTGTGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1790
 Qy 1741 GCGCCGCGTGGGAGCGCCCTTTGAGGAGCAGCAGCTTCAGACCTGTGTGAGGAGCA 1800
 Db 1791 GCGCCGCGTGGGAGCGCCCTTTGAGGAGCAGCAGCTTCAGACCTGTGTGAGGAGCA 1850
 Qy 1801 GTACTGAAAGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1860
 Db 1851 GTACTGAAAGTCTGTCCAGGCTCCACCTTCCTGCCCCGATGACCTCAGCTGGGTGTG 1910
 Qy 1861 CTTAGACCTCCCGTAAACCAATTCCTGAGGAGCCCATTCCTGAGCTCCCATGACCAT 1920
 Db 1911 CTTAGACCTCCCGTAAACCAATTCCTGAGGAGCCCATTCCTGAGCTCCCATGACCAT 1970
 Qy 1921 GGGAGGTGGGCGCTCAATCTAGAGCCCTTCCTGAGGAGGCGGTGAGGAGGAGGAGG 1979
 Db 1971 GGGAGGTGGGCGCTCAATCTAGAGG-CTTCCCTGTCAGAGAGGCGGTGAGGAGGAGG 2029
 Qy 1980 CATTCAAGAGTCCATCCCTCCCGTTGAGTGAAGCCTGTGGGAGGCTTTCCCT 2039
 Db 2030 CATTCAAGAGTCCATCCCTCCCGTTGAGTGAAGCCTGTGGGAGGCTTTCCCT 2089
 Qy 2040 ATCCACAGGCGGTGTGTGTGT 2061
 Db 2090 ATCCACAGGCGGTGTGTGTGT 2111
 RESULT 7
 AACT8180
 ID AACT8180 standard; cDNA: 2432 BP.
 AC AACT8180;
 DT 08-FEB-2001 (first entry)
 DE Human cancer associated gene sequence SEQ ID NO:574.
 XX Human; cancer associated gene: cancer antigen; detection: cancer;
 KM diagnosis: cytostatic; proliferative; vulnary; immunomodulator;
 KM antidiabetic; antihypertensive; antirheumatic; antidiabetic; antidiabetic;
 KM antidiabetic; antihypertensive; antirheumatic; antidiabetic; antidiabetic;
 KM dematologic; neuroprotective; thrombolytic; coagulant; neurologic;
 KM vasotropic; antiproliferative; angiogenic; gene therapy; inflammation;
 KM immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KM allergic reaction; graft versus host disease; organ rejection;
 KM haemostatic; thrombolytic; cardiovascular disorder; infection;
 KM neurological disease; drug screening; ss.
 OS Homo sapiens.
 OS WO20005350-A1.
 PD 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US05882.
 PF 12-MAR-1999; 99US-0124270.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 XX PI

XX WP1: 2000-587533/55.
 DR P-PSDB: AAB43971.
 XX Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -
 PT
 PS Claim 1: Page 1097-1098; 2352pp; English.
 XX
 CC AACT7607 to AACT8180 encode the human cancer associated proteins given
 CC in AAB43971 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antihypertensive; antirheumatic; antidiabetic;
 CC antidiabetic; antihypertensive; antirheumatic; antidiabetic;
 CC dematologic; neuroprotective; coagulant; thrombolytic; coagulant;
 CC neurologic; vasotropic; antiproliferative; angiogenic; gene therapy;
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells; to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection; modulate haemostatic or thrombolytic activity; modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AACT8180 to
 CC AACT7607 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.
 XX
 S0 Sequence 2432 BP; 460 A; 764 C; 707 G; 496 T; 5 other;
 Query Match 96.1%; Score 2014; DB 21; Length 2432;
 Best Local Similarity 99.2%; Pred. No. 0; Mismatches 15; Indels 2; Gaps 2;
 Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
 Qy 1 CGCAGGAGACCATGTGAGCCCTGTGAGCTGGTGGCTTTAAGCAGGCGGTGTGCT 60
 Db 176 CGCAGGAGACCATGTGAGCCCTGTGAGCTGGTGGCTTTAAGCAGGCGGTGTGCT 235
 Qy 61 GGAAGCGGTGGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 236 GGAAGCGGTGGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 295
 Qy 121 GCGAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 296 GCGAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 355
 Qy 181 CTGGGTGGCCCTGCGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 356 CTGGGTGGCCCTGCGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
 Qy 241 GTTCAGGAGGATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 416 GTTCAGGAGGATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
 Qy 301 CACTGTGTCCAGGCGGTTCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 476 CACTGTGTCCAGGCGGTTCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
 Qy 361 GGTAAACATCCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 536 GGTAAACATCCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
 Qy 421 TCCAGTGTCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 596 TCCAGTGTCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
 Qy 481 TGTGTGAAGACAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 656 TGTGTGAAGACAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715

CC ET-1 and ET-2 were isolated from rat kidneys and their amino acid
CC sequences determined. A full length rat ET cDNA (AA014338) was obtcd.
CC by screening a rat kidney cDNA library in lambda gt10 with PCR
CC generated ET probes. These probes were also used to obtain the mouse
CC ET gene (AA014340) from a mouse T-cell genomic library.
CC ET DNA was also obtained from human sources (AA013333).
CC An anti-sense ribonucleic acid molecule complementary to the
CC indicated fragment in the features is also claimed.
CC ET-1 is a bifunctional growth regulator, capable of stimulating
CC the growth of some cell types while inhibiting the growth of others.
CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
CC bioactivity. In contrast, however, ET-2 is apparently not capable of
CC eliciting the growth stimulatory activity characteristic of ET-1 and,
CC in fact, antagonises this ET-1 activity.
CC See also, AA014338-40, AA014952-53, AAR14328-9 and AAR15315-20.

XX Sequence 1779 BP: 304 A; 578 C; 547 G; 350 T; 0 other:

Query Match 83.8%; Score 1756.6; DB 12; Length 1779;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 13 ATGTGACCCCTGTGAGTGGGGTGGCTTAACAGCAGGAGGTGGTGGTGAACGGGGTGC 72
DB 1 ATGTGACCCCTGTGAGTGGGGTGGCTTAACAGCAGGAGGTGGTGGTGAACGGGGTGC 60
OY 73 CCAGATGGTCAATTTGCTGCTGTGGCTGTGCTGTGACCCCGAGAGCCAGTACAGC 132
DB 61 CCAGATGGTCAATTTGCTGCTGTGGCTGTGCTGTGACCCCGAGAGCCAGTACAGC 120
OY 133 TGTCTCCCTGCCCTTCTGTGCAATAATGGCCACACACTGAGCAGGCATCTGGGTGGCCC 192
DB 121 TGTCTCCCTGCCCTTCTGTGCAATAATGGCCACACACTGAGCAGGCATCTGGGTGGCCC 180
OY 193 TGCCAGGTTGATGGCCACATGCTCTGCGGACCTCTGCATCTTAACTGTCAGAGGACT 252
DB 181 TGCCAGGTTGATGGCCACATGCTCTGCGGACCTCTGCATCTTAACTGTCAGAGGACT 240
OY 253 TCCAGTCTGTGCCCCCTTCCACAGAGCCGCTGGCAGTCGGGAGTGGCCATCACTGTGCCCA 312
DB 241 TCCAGTCTGTGCCCCCTTCCACAGAGCCGCTGGCAGTCGGGAGTGGCCATCACTGTGCCCA 300
OY 313 CGGGCTTCCACTGACATGACAGACGGGCGATCTCTTCCAAAGTCAAGTTAACTATCC 372
DB 301 CGGGCTTCCACTGACATGACAGACGGGCGATCTCTTCCAAAGTCAAGTTAACTATCC 360
OY 373 GTGGGTGCATTCAGATGCTGTAGTCAATGCAATGCCGAGACTTCTCCACGTGCTGT 432
DB 361 GTGGGTGCATTCAGATGCTGTAGTCAATGCAATGCCGAGACTTCTCCACGTGCTGT 420
OY 433 GTTATGTCGATGGCTCTGTGGGGTGTCTGCCCATGCCCCAGGCTTCTGTGTGAAGAC 492
DB 421 GTTATGTCGATGGCTCTGTGGGGTGTCTGCCCATGCCCCAGGCTTCTGTGTGAAGAC 480
OY 493 AGGGTGCATGCTGTCCGACAGGTGCTTTCGCGACCTGTTCACACCCGCTGCATCACA 552
DB 481 AGGGTGCATGCTGTCCGACAGGTGCTTTCGCGACCTGTTCACACCCGCTGCATCACA 540
OY 553 CCCAGGGACACCCACCCCTGTGCAAGAAGTCCCTGCCAGAGAGTCAACAGGGCAGTG 612
DB 541 CCCAGGGACACCCACCCCTGTGCAAGAAGTCCCTGCCAGAGAGTCAACAGGGCAGTG 600
OY 613 GCCCTGTGCAGCTCGGTATGTCTCGGACGACAGCGTCCCGGTGCTCTGATGGTCTAC 672
DB 601 GCCCTGTGCAGCTCGGTATGTCTCGGACGACAGCGTCCCGGTGCTCTGATGGTCTAC 660
OY 673 TGTCTTGACCTGCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCCACGCCACTGTGTC 732
DB 661 TGTCTTGACCTGCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCCACGCCACTGTGTC 720
OY 733 TCCGATCACTGCATGCTGCCGCCAAGACACTGTGTGACCTGATCCAGAGTAAGTGC 792
DB 721 TCCGATCACTGCATGCTGCCGCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC 780

OY 793 CTCTCCAGGAGAAAGCTACACGAGACCTCTCTCACTAAGTGTGCTGCGCACACAGTGGGC 852
DB 781 CTCTCCAGGAGAAAGCTACACGAGACCTCTCTCACTAAGTGTGCTGCGCACACAGTGGGC 840
OY 853 GATGTGAATGTGACATGAGAGTGAAGTGGCCAGATGGCTTATACCTGTGCTGCTTACAG 912
DB 841 GATGTGAATGTGACATGAGAGTGAAGTGGCCAGATGGCTTATACCTGTGCTGCTTACAG 900
OY 913 TGGGGGGCTGGGGGTGCTGCTTATACCAAGGTGTGTCTGTGAGGACCATATCAC 972
DB 901 TGGGGGGCTGGGGGTGCTGCTTATACCAAGGTGTGTCTGTGAGGACCATATCAC 960
OY 973 TGTCTGCCGGGGGTTTACGTGTGACACGAGAGAGGTACCTGTGAAACAGGGGCCCCAC 1032
DB 961 TGTCTGCCGGGGGTTTACGTGTGACACGAGAGAGGTACCTGTGAAACAGGGGCCCCAC 1020
OY 1033 CAGTGGCTTGGATGAGAGAGGCCCCAGCTACCTCAGCTGCGACAGCCCAAGCCTTG 1092
DB 1021 CAGTGGCTTGGATGAGAGAGGCCCCAGCTACCTCAGCTGCGACAGCCCAAGCCTTG 1080
OY 1093 AAGAGATGTCCCTGTGATATGTCAAGAGCTGTCCCTCTCCGATACCTGTGGCAA 1152
DB 1081 AAGAGATGTCCCTGTGATATGTCAAGAGCTGTCCCTCTCCGATACCTGTGGCAA 1140
OY 1153 CTCACGTCTGGGGAATGGGGGTGCTGTCCAAATCCAGAGCTGTCTGTGCTGCGAGCAC 1212
DB 1141 CTCACGTCTGGGGAATGGGGGTGCTGTCCAAATCCAGAGCTGTCTGTGCTGCGAGCAC 1200
OY 1213 CAGCACTGCTGCCCCAGCAGTACACGTGTGTAGTGAAGGGGCACTGTCAAGAGAAAC 1272
DB 1201 CAGCACTGCTGCCCCAGCAGTACACGTGTGTAGTGAAGGGGCACTGTCAAGAGAAAC 1260
OY 1273 GAGATGCTGGGTGAGCTGGAAGATGTGCTGCGCGCCGCGGTCTTATCCACCCAGA 1332
DB 1261 GAGATGCTGGGTGAGCTGGAAGATGTGCTGCGCGCCGCGGTCTTATCCACCCAGA 1320
OY 1333 GACATGGCTGTGACACACACACAGCTGCCCCGTGGGGGGAACCTGTGCCAGGCCAG 1392
DB 1321 GACATGGCTGTGACACACACACAGCTGCCCCGTGGGGGGAACCTGTGCCAGGCCAG 1380
OY 1393 GGTGGAGCTGGGGCTGTGCTGCAAGTGTGCCCCATGTGTGTCTGTGAGAGATGCCAGCAC 1452
DB 1381 GGTGGAGCTGGGGCTGTGCTGCAAGTGTGCCCCATGTGTGTCTGTGAGAGATGCCAGCAC 1440
OY 1453 TGTCTCCGGCTGTGACATGCACTGCAACAGTGAAGGCTCATCTCTCGAGAGAAAGTGGTC 1512
DB 1441 TGTCTCCGGCTGTGACATGCACTGCAACAGTGAAGGCTCATCTCTCGAGAGAAAGTGGTC 1500
OY 1513 TCTGCCAGCCTGACCTTCTGTGGCCGCTAGCCCTCACGTGGGTGTGAAGACGTGGAG 1572
DB 1501 TCTGCCAGCCTGACCTTCTGTGGCCGCTAGCCCTCACGTGGGTGTGAAGACGTGGAG 1560
OY 1573 TGTGGGGAAGACACTTGTGCGCATATGAACAGACACTGCTGCCAGACACAGAGGCC 1632
DB 1561 TGTGGGGAAGACACTTGTGCGCATATGAACAGACACTGCTGCCAGACACAGAGGCC 1620
OY 1633 TGGGCTGCTGTCTCCCTACGCGCAGAGGCTGTGTGTGTGATGCGGCGCACTGTCTCT 1692
DB 1621 TGGGCTGCTGTCTCCCTACGCGCAGAGGCTGTGTGTGTGATGCGGCGCACTGTCTCT 1680
OY 1693 GCTGGCTTCCGCTGCGACAGCAGAGGGGTACCAAGTGTGTGCGCAGAGAGGCCCGCGCTGG 1752
DB 1681 GCTGGCTTCCGCTGCGACAGCAGAGGGGTACCAAGTGTGTGTGCGCAGAGAGGCCCGCGCTGG 1740
OY 1753 GACGCCCTTTGAGGAGACCCAGCCTTGTGAGACAGCTGCTG 1791
DB 1741 GACGCCCTTTGAGGAGACCCAGCCTTGTGAGACAGCTGCTG 1779

RESULT 9
AAH16370
ID AAH16370 standard; cDNA: 1630 BP.

Db	371	G	-ATAACCCCTTGGGGTGTGTCACATGTCCTGGAGGCCAGTTTGAATGCTCGACTCT	427
Oy	421	TTCCACGCTGCTGTATAGTGTGATAGGCTCTCGTGGGGGGTGTGTCCCATAGTCCCAAGCTTCC	480	
Db	428	GCACCTCTCTCATTTATGTTGAAGTGTTCGTGGGGATGTTGTCTCCATATGCCCGAGCTCTT	487	
Oy	481	TGCTGTGAAGACAGGGTGTGCATGCTGTGCCGACGGTACCTCTTGTGCACAGCTGTATCACACC	540	
Db	488	TGCTGTGAAGACAGAGTGTGCATTTGCTGTGCCATATGGGGCTCTCTGTACCTGTGTACACA	547	
Oy	541	CGCTGTACACACCCACGCGCACCCACCCTTGGCAAAAGAGCTCCCTGCCACAGAGACT	600	
Db	548	CGATGCGTTTACCCACGCGGACCCACACCTTACTAAAGATGTCTCTGCACAAAAGACC	607	
Oy	601	AACAGGGCAGTGGCCCTTGTCCAGTCCGGTCAATGTATGCCGGACCGACGTCGCGGTGCCCT	660	
Db	608	AACAGGGCAGTGTCTTGTTCCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	667	
Oy	661	GATGGTTCCTACCTGCTGTGAGCTGCCAGTGGAGATAGTGGTGTGCTGCCCAATGCCCAAC	720	
Db	721	GCCACGCTGCTCTCGATACCTGTGCATCTGCTCCGCCCAACACATGCTGTGTATACCTGATC	780	
Oy	781	CAGAGTAAGTGCTCTCTCCAAAGAAAGACGTACACAGGACCTCTGCATCTAAGCTGTGCTGCG	840	
Db	788	CAGAGTAAGTGCTCTATCA --- AATACTAACACAGGATCTCTGTGACCAAGCTGTGCTGGA	844	
Oy	841	CACACAGTGGGCGATGTGAATTTGACATGTGAGGTGAGCTGCCAGATGGCTTTTACCTGC	900	
Db	845	TACCCAGTGAAGAGGTGAATGTGGATGTGAGATGGATGTGAGCTGCCCTGAAGATTTTACCTGC	904	
Oy	901	TGCCGTCTACAGTGTGGGGGGCTGGGGGCTGCGCCCTTTTACCAAGGCTGTGTCTGTGAG	960	
Db	905	TGCCGCTCTACACTGTGGGGCTGGGGCTGCTGTCTCATTGTGCAAGGCGCTGTGTGTGTGAG	964	
Oy	961	GACCATATACACTGTCTGTCCCGCGGGGTTTTACGTGTGACACGCAAGAGGGTTACCTGTGAA	1022	
Db	965	GATCATCTTACTTGTCTGCTCCCGCAGGGTTTACGTGTACACAGAGAAAGAACCTGTGGAA	1022	
Oy	1021	CAGGGGGCCCCACAGGTGCCCCGTGGATGGAAGAAAGGCCCACTCACTCACTCACTGCGCAAC	108	
Db	1025	ATGGGTATCTCTTCAAGTATACCTGTGATGAAGAAAGGTCTATAGCCCCCTCGCCCTGTGCAGAC	108	
Oy	1081	CCACACGCTTTGAAGAGAGATGTCCCTGTGTATATGTACAGACAGCTGTCCCTCTCCGAT	114	
Db	1085	CCACAGATCTTTGAAGAGATATACACCTTGTGATGACTTCACTAGTGTCTCTACAAACAAAT	114	
Oy	1141	ACCTGTCTCCCACTACGTCTGTGGGAATGGGGCTGTCTGTCCAAATCCACAGAGCTGTCTGC	120	
Db	1145	ACCTGTCTCCAACTCAATTTCTGGGGAGATGGGGCTGTCTGTCCAAATCCACAGAGCTGTCTGC	120	
Oy	1201	TGCTTGTGACACACAGCACTGTGTGCCCCACAGAGATACACAGTGTGATGTGAGGGGACAGTGT	126	
Db	1205	TGCTGTAGACAACAGCAATGTGTGCCCTCAAGGCTTTCACATGTCTGTGTGTGTGTGTGTGTGT	126	
Oy	1261	CAGCAGGAGACCGAGATGTGTGCTGTGAAGTGTGAGAGATGCTCTGCCCGCGCGGTTCCTTA	1322	
Db	1265	CAGAGGAGAGACAAATGTGTGTGCTGTGCCCTGTGAGAGATTTACCTGTGCCCGCGCAGAACCCCG	1322	
Oy	1321	TGCCACCCACAGACATGTGGCTGTGACACAGACACACAGCTGCCCGGTGGGGGACCACTTGC	138	
Db	1325	CTCCAAATTTGGAGATATGTGTTGTGTACACAGCATACACAGCTGTGCCAGTAGAGGGCAAACTGTG	138	
Oy	1381	TGCCGAGCCAGAGGTGGAGCTGGGACTGTGCCAGTGTGCCCATGTGTGTGTGTGTGTGTGTGTGT	144	
Db	1385	TGCCCAACCTCTCAAGGGAGATTTGGGGCTGTGCTGCCAGCTGTGCCCATGTGTGTGTGTGTGT	144	
Oy	1441	GATGCCAGACATCTGTGCCCGGGCTGTACACCTGTGCAACCTGAAAGCTGCATCTCTGTGAG	150	
Db	1445	GATGCCAGACATCTGTGCCCGGGCTGTACACCTGTGCAACCTGAAAGGCTGGAAGCTGTGTGTGT	150	

Oy	1501	AAGGAAGTGGCTCTGCGCCACGCTTCCTTGAGGCCGTAGCTGGGTGG	1560
Dd	1505	AAGCATGTGCATTTTATTATCCAGCCTCCGTCCTCTCAACCCTGAGGTTGG---	1566
Oy	1561	AAGGACGTGAGTGTGGGGAAGAAGACACTTGTGCATGATTAACAGACGCTGTGCCGAGNC	1620
Dd	1561	--GAAATGTGAGTGTGGGAAGAGGCAATTTCTGCGCATGATTAACAGACGCTGTMAAGNC	1618
Oy	1621	AACCGACAAGGCTGTGGCCTGTGCTGTCCCTACGCCAGGCGCTGTGTGTCTGATCGCGC	1680
Dd	1619	AGTGAAGAGATGTGGGCTGTGCTGTCCCTAACAAAGGAGTGTGCTGTGAGATGAGAGT	1678
Oy	1681	CACGTGCTCTGCTGTGCTTCCTCCGTCGACAGAGGAGGTATCCAAAGTGTGTGGCAGGGG	1740
Dd	1679	CACBTGTGCCCGGTGGCTTCCTCACTGTTCACGCAAGGAGCAACAGTGTGTGGAAAAAG	1738
Oy	1741	GCCCCGCGCTGGGAGCGCCCTTGTGAGGAGCACAGCCTTGTAGACAGCTGCTGTGAGGAGCA	1800
Dd	1739	ATTCCTGCTGGACATGTTTGTGAGGAGATCCGGTCCCAAACCGCTACTGTAAAGGAAG	1798
Oy	1801	GTACTGAA-----GACTGTGACAGCCTTGTGGGACACCCCACACTGGGAGGTTGCCCTGCTC	1855
Dd	1799	GCTACAGACTTAAAGAACTCCACAGTCTGTGGAAACCTGTGTCGAGGGATACCACTACTC	1858
Oy	1854	AGGCTCCCTAGACATCCGCCCTTAACCAATTCCTCCCTGGACCCCATTTCTGAG-CTGCC	1912
Dd	1859	AGGCTCCCTAGACATGCTCTCTCCCTTAACGTTCTCCGGCTACTCATCTGTGATACCT	1918
Oy	1913	ATCACATGAGGAGGTGGGGGCTCAATCTAAGGCCCTTCCCTGTCAAGAAAGGGGGTTGAG-	1972
Dd	1919	ATCACATGAGGAGGTGGAGGCTCAATAACTTAACCTTCTTTTAGAAAAGAAAGAGTGTGG	1978
Oy	1972	CAAAAGCCCATTTACAAGCTGCGCATCCCTCCCGTTTCACTGAGGACCTGTGGCCAAGTGC	2033
Dd	1979	CAAAAGCCCGCTATCAAACTGACCATTTCTTCCGGTTTCTGTGAGACCTGTGGCCAGGTGC	2038
Oy	2032	TTTTCCCTATCCACAGGGAGTGTGTGTGTGTGGGTGG	2069
Dd	2039	TCTTCCGAGCCACAGAGTGTGTGTGTGTGTGTGTGTG	2076
<hr/>			
RESULT 11			
ID	AAV82824		
ID	AAV82824	standard; cDNA; 2137 bp.	
xx	AAV82824;		
AC			
xx			
DT	15-MAR-1999	(first entry)	
xx			
DE			
Mouse GP88 autocrine growth factor cDNA.			
xx			
KW	GP88; granulin; epith1lin; mouse; growth factor; autocrine; tumour;		
KM	cancer; viral infection; antagonist; therapy; diagnosis; ss.		
xxx			
OS	Mus sp.		
xx			
Key		Location/Qualifiers	
FH	CDS	23..1792	
FT		/lag-a	
FT		/transl_except- (pos:44..45, aa:ile)	
FT		/transl_except- (pos:182..184, aa:asp)	
FT		/transl_except- (pos:1151..1153, aa:Cys)	
FT		/transl_except- (pos:1340..1342, aa:Leu)	
xx			
PN	W09852607-AI.		
xx			
PD	26-NOV-1998.		
xx			
PP	22-MAY-1998;	98MO-US10555.	
PR	16-DEC-1997;	97US-0991862.	
PR	23-MAY-1997;	97US-0863079.	

Key	Location/Qualifiers
PH	23.1792
FT	/tag= a
FT	/transl_except= (pos:44..45, aa:Ile)
FT	/transl_except= (pos:182..184, aa:Asp)
FT	/transl_except= (pos:1151..1153, aa:Cys)
FT	/transl_except= (pos:1340..1342, aa:Leu)
XX	
PN	W09852607-A1.
PD	26-NOV-1998.
XX	
PF	98WO-US10555.
XX	
PR	16-DEC-1997;
PR	23-MAY-1997;
PR	97US-0991862.
PR	97US-0863079.

xx (SERR/) SERRERO G.

xx Serrero G:

xx WPI: 1999-045276/04.

xx P-PSDB: AAM85474.

xx Composition containing antagonist of growth factor GP88 - useful for
xx treating cancer and viral diseases and also for diagnosing disease
xx from altered GP88 expression

xx Example 5; Fig 8A-D; 86pp; English.

xx This murine cDNA sequence includes a coding region for GP88 (see
xx AAM85474), an 88 kDa glycoprotein autocrine growth factor and
xx epithelin/granulin precursor that is expressed in a tightly
xx regulated manner in normal cells, is overexpressed and upregulated
xx in highly tumorigenic cells derived from normal cells, and which
xx acts as a stringently required growth stimulator for the
xx tumorigenic cells. Inhibition of GP88 expression or action in the
xx properties of the overproducing cells. Murine GP88 cDNA was
xx isolated from the highly tumorigenic PC cell line cDNA library
xx using a probe obtained by PCR using primers based on isolated GP88
xx peptides. Antagonists to GP88 are used to treat diseases
xx associated with increased expression of GP88, particularly cancer
xx but also viral infections. Fragments of GP88 are used to raise
xx and for delivering toxins or other compounds to GP88-expressing
xx cells) and to screen for antibodies. Antisense oligonucleotides
xx can also be used as antagonists. Methods are provided for
xx diagnosing disease, or determining susceptibility to disease,
xx resulting from altered GP88 activity.

xx Sequence 2137 BP; 443 A; 608 C; 583 G; 503 T; 0 other;

xx Query Match 57.5%; Score 1204.8; DB 20; Length 2137;
xx Best Local Similarity 75.8%; Pred. No. 1e-291;

xx Matches 1575; Conservative 0; Mismatches 482; Indels 21; Gaps 6;

QY 1 GCGAGGACACATGTGACACCTGCTGAGCTGGCTTACAGACAGGCGTGGCT 60
DB 11 GCGACACAGACATGTGGCTCTGATGAGCTGGCTTACAGACAGGCGTGGCT 60
QY 61 GGAAGCGGCTGCGAGATGTCAGTTCGCGCTGGCTGCTGCTGAGACCCGGAAGA 120
DB 71 GGAACACAGTGTCCAGATGGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 130
QY 121 GCGACCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 131 GCGACCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
QY 181 CTGGGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 191 CTAGATGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
QY 241 GTCTCAGGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 251 GTGCTGGGACTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 301 CACTGCTGCGCCAGGCGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 311 CACTGCTGCGCCAGGCGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
QY 361 GGTAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 371 G---ATAACCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
QY 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 428 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487

QY 481 TGCTGTGAAGACAGAGTGCATGCTGTCCGACAGGCTTCTGCGACCTGGTTACACC 540
DB 488 TGCTGTGAAGACAGAGTGCATGCTGTCCGACAGGCTTCTGCGACCTGGTTACACA 547
QY 541 CGCTGATCACACCCAGGCGACCCCTGCGAAGAAAGCTCTGCGCAGAGACT 600
DB 548 CGATGCTTTCACCCAGGCGACCCCTGCGAAGAAAGCTCTGCGCAGAGACT 607
QY 601 AACAGGACAGTGGCTTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 608 AACAGGACAGTGGCTTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 661 GATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 668 GATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 728 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
QY 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 788 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
QY 841 CACACAGTGGCGCATGTGAATGTGACATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 845 TACCAAGTGAAGAGGAGTGAATGTGACATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
QY 901 TGCGGTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 905 TGCGGTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
QY 961 GACCACTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 965 GATCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
QY 1021 CAGGCGCGCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1025 ATGGATATCTCCAAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
QY 1081 CCAACAGCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1085 CCAACAGCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
QY 1141 ACCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1145 ACCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
QY 1201 TGCTGAGACACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1205 TGCTGAGACACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
QY 1261 CAGCGAGAGAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1265 CAGCGAGAGAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
QY 1321 TCCACCCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1325 TCCACCCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
QY 1381 TGCCGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1385 TGCCGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1441 GATGCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1445 GATGCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
QY 1501 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1505 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

QY 733 TCCGATCACTGCTGCTGCCCCAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC 792
 DB 728 TCCGACACACTGCTGCTGCCCCAGAGACACTGTATGTGACCTGATCCAGAGTAAGTGC 777
 QY 793 CTCCTCAAGAGAACGCTACACAGGACCTCTGACTAAGCTGCTGCGCACAGTGGGC 852
 DB 778 ATATCAAGAGTAAC---ACACAGATCTCATGACCAAGCTCCGTGATACCCAGTAAT 834
 QY 853 GATGGAATGATGATGAGGTGAGCTGCCAGATGGCTATACCTGGCTGGCTGATACG 912
 DB 835 GAGGGAAGTGGATGAGGTGAGCTGCTGATGGCTGATACCTGGCTGGCTGATACG 894
 QY 913 TCGGGGGCTGGGGCTGCTGCTGCTTTTACCCAGGCTGTGTGTGTGAGAGCCACATAC 972
 DB 895 ACTGGGGCTGGGGCTGCTGCTGCTATTCACCAAGGCTGTGTGTGTGAGAGCCACATTC 954
 QY 973 TGTCTCCCGGGGCTTACGTGTACACAGCAAGAGGCTGCTGTAACAGGGGCCCCAC 1032
 DB 955 TGTCTCCCGGGGCTTACGTGTACACAGCAAGAGGCTGCTGTAACAGGGGCTGCTT 1014
 QY 1033 CAGGTGCTGGATGAGAGAGGCCCCAGCTCAGCTCAGCTCCAGACCCACAGCCTTG 1092
 DB 1015 CAGGTACCTGGATGAGAGAGGCTCAGGCTCCTCAGCTCCAGACCCACAGATCTTG 1074
 QY 1093 AAGAGAGATGCTCCCTGTGATATGTACAGACAGCTGCTCCCTCCGATACCTGCTG 1152
 DB 1075 AAGATGATGCTCCCTGTGATATGTACAGACAGCTGCTCCCTCCGATACCTGCTG 1134
 QY 1133 CTCACGCTGGGAGTGGGGCTGCTGCTCCAAATCCAGAGGCTGCTGCTGCTGACAC 1212
 DB 1135 CTCACGCTGGGAGTGGGGCTGCTGCTCCAAATCCAGAGGCTGCTGCTGCTGACAC 1194
 QY 1213 CAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
 DB 1195 CAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
 QY 1273 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1332
 DB 1255 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
 QY 1333 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1392
 DB 1315 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
 QY 1393 GGTGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
 DB 1375 AAGGGAATGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
 QY 1453 TGTGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512
 DB 1435 TGTGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494
 QY 1513 TGTGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1572
 DB 1495 TGTGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
 QY 1573 TGTGGAAGAGACACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1632
 DB 1549 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
 QY 1633 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1692
 DB 1609 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1668
 QY 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1752
 DB 1669 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728
 QY 1753 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
 DB 1729 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1767

RESULT 13
 ID AAQ14340
 AAQ14340 standard: DNA: 1767 BP.
 AC AAQ14340;
 AC 17-JAN-1992 (first entry)
 DE Mouse epithelin precursor.
 DE ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT misc_RNA 8..1774
 FT /*tag= a
 FT /note= "claim 29, page 56"
 PN MO9115510-A.
 PD 17-OCT-1991.
 PF 03-APR-1991; 91WO-US02321.
 PF 13-MAR-1991; 91US-0083796.
 PR 03-APR-1990; 90US-0504508.
 XX (BRIM) BRISTOL-MYERS SQUIB.
 PA Shoyab M, Plowman GD;
 PI WPI: 1991-325168/44.
 DR P-PSDB: AAR14327.
 XX
 PT New cysteine-rich growth modulating proteins, epithelins - useful
 PT as inhibitors of neoplastic cell growth and to promote wound
 PT healing and treat psoriasis
 PS Disclosure: Fig 23; 97pp; English.
 CC ET-1 and ET-2 were isolated from rat kidneys and their amino acid
 CC sequences determined. A full length rat ET cDNA (AAQ14338) was obtd.
 CC by screening a rat kidney cDNA library in lambda gt10 with PCR
 CC generated ET probes. These probes were also used to obtain the mouse
 CC ET gene (AAQ14340) from a mouse T-cell genomic library.
 CC An anti-sense ribonucleic acid molecule complementary to the
 CC indicated fragment in the features is also claimed.
 CC ET-1 is a bifunctional growth regulator, capable of stimulating
 CC the growth of some cell types while inhibiting the growth of others.
 CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
 CC bioactivity. In contrast, however, ET-2 is apparently not capable of
 CC eliciting the growth stimulatory activity characteristic of ET-1 and,
 CC in fact, antagonises this ET-1 activity.
 CC See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
 CC
 SO Sequence 1767 BP: 360 A: 503 C: 492 G: 412 T: 0 other:
 Query Match 52.9%; Score 1107.4; DB 12; Length 1767;
 Best Local Similarity 77.6%; Pred. No. 2.3e-267;
 Matches 1381; Conservative 0; Mismatches 386; Indels 12; Gaps 3;
 QY 13 ATGTGGACCTGTGATGCTGGGTGCTTACAGAGAGGCTGTGGTGAAGCGGTGC 72
 DB 1 ATGTGGGTCTGTGATGCTGGGTGCTTACAGAGAGGCTGTGGTGAAGCGGTGC 60
 QY 73 CCAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
 DB 61 CCAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 133 TGTGCTCCCGTCCCTTCTGGAACAATGGCCACACACTGAGCAGGCAATGTGGGTGCC 192

Db 121 TCCCTTAACCCCTTCTGGACACATGGCCCTAGAAATAACAGGCATCATCTAATGCTCC 180
Qy 193 TCCAGGTTGATGATCCACTGCTGCGGGCCACCTCCATCTTTACCTTCAGGACT 252
Db 181 TCCAGACCCATGGGCACAGTCTGCTGGCTATCTTCTCTCTCACTGTCTGGAGCT 240
Qy 253 TCCAGTTCCTGCCCCCTCCAGAGCCCTGGCATGGGGGATGGCCATCTGTCGCCA 312
Db 241 TCCACTCTGCTGCCCTCTCTAAGGGTGTGTCTGTGGTGGTACCACTGCTCCCC 300
Qy 313 CCGGCTTCCTCACTGACAGTCCAGACGGCGATCTGCTTCCAAAGATCAGGTAACTCC 372
Db 301 CAGGCTTCCTCACTGACAGTCCAGAGGAAATCTGCTTCCAAATGTCAG---ATAACCCC 357
Qy 373 GTGGTGCATCCAGTGGCCCTGATAGTCAATGCAATGCCCCGAGCTTTCACAGTCTGT 432
Db 358 TTTGGTGCCTGCTCACTGCTCTGGAGCCAGTTTGAATGTCTGACTCTGCTCACTGCTCC 417
Qy 433 GTTATGTCTGATGGCTCTGCGGGGTCTGCCCCATGCCCCAGGCTTCTGCTGTAAGAC 492
Db 418 ATTATGTTGATGGTTCGCGGGGATGTGTCTCCATGCCCCAGGCTTGTGTGTAAGAC 477
Qy 493 AGGCTGCACTGCTGTCCGACGCTGCTTCTGCGACTGCTTACACACCCGCTGATCACA 552
Db 478 AGAGTGCATGCTGTGTCCTCATGGGCTCTCTGACCTGTTTACACACAGATGCGTTTGA 537
Qy 553 CCCACGGGACCCACCCCTGGCAGAAAGATCTCCCTGCCAGAGGACTTAACAGGGGACGT 612
Db 538 CCCAGGGGACCCACACCTACTAAAGAAATTCCTCTGCAAAAAGACAAACAGGGGACGT 597
Qy 613 GCTTGTCCAGCTGCGTCAATGTCTCCGACGACGGTCCCGGTGCCGTGATGTTCTAC 672
Db 598 TCTTGTCCCTTTTGT 657
Qy 673 TGCCTGAGCTTCCAGTGGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 658 TGCCTGAGCTTCCAGTGGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
Qy 733 TCCGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
Db 718 TCCGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Qy 793 CTCTCCAAAGAGACGCTACACAGGACCTCTCACTAAGCTCTGCTGCTGCTGCTGCTG 852
Db 778 CTATCCA---AGAACTACACACAGGATCTCTGACCAAGCTGCTGATACCAAGTGAAG 834
Qy 853 GATGGAATGTGACATGGAAGTGAAGTCCAGATGCTATACCTGCTGCTGCTGCTGCTG 912
Db 835 GAGGTGAAGTGGACATGGAAGTGAAGTCCCTGAAAGATATACCTGCTGCTGCTGCTG 894
Qy 913 TCGGGGCTGGGGTGTGCTGCTTTCACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 972
Db 895 ACTGGGCTGGGGTGTGCTGCTTTCATTTGCTCAAGGCTGTGTTGTGATGATACATTTCA 954
Qy 973 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
Db 955 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1014
Qy 1033 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092
Db 1015 CAAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Qy 1093 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1152
Db 1075 AAGATGATACACCTTGTGATACCTTCACTAGTGTCTTCAAAACATATCTGCTGCTG 1134
Qy 1153 CTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
Db 1135 CTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Qy 1213 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272

Db 1195 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
Qy 1273 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1332
Db 1255 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
Qy 1333 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1392
Db 1315 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
Qy 1393 GGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
Db 1375 AAGGAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
Qy 1453 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512
Db 1435 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494
Qy 1513 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1572
Db 1495 TTTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
Qy 1573 TGTGGGGAAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1632
Db 1549 TGTGGAAAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
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AC
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DE
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OS
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Search completed: February 21, 2003, 13:05:06
Job time : 486 secs

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DEFINITION M75161
ACCESSION M75161.1 GI:183612
VERSION granuln.
KEYWORDS Homo sapiens (tissue library: Clontech HL1058b) adult bone marrow
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2095)
AUTHORS Bhandari,V., Palfrey,R.G. and Bateman,A.
TITLE Isolation and sequence of the granuln precursor cDNA from human
bone marrow reveals tandem cysteine-rich granulin domains
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1715-1719 (1992)
MEDLINE 92179253
PUBMED 1542665
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Qy	2041	TCCACAGGGGTGTTGTGTGGGTGTGCTTTCATATAAGTTTGCAATTTCTT	2095
Db	2041	TCCACAGGGGTGTTGTGTGGGTGTGCTTTCATATAAGTTTGCAATTTCTT	2095

[illegible]

FEATURES	JOURNAL	REMARK	COMMENT
	<p>Strausberg, R. Direct Submision Submitted (10-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</p>	<p>NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm.tmc.edu Villalon, D. K., Luna, R.A., Hale, S.M., Huiyik, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.</p>	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://linlge.linl.gov Series: IRAX Plate: 12 Row, a Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10435243. Location/Qualifiers</p>

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FEATURES      LOCATION/QUALIFIERS      MATCHED MINIMA Y1: 104352483
SOURCE        1. 2132

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Q	y	901	TGCGGTCTACAGTGGGGGGCTGGGGCTGTGCTCCCTTAACCAAGCTGTGTGCTGTAG	960
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Q	y	1021	CAGGGGCCCCACAGGTGCCCTGTGATGTGAGAGAGGCCCAAGCTCACCTCAGCTGCCACAC	1080
D	b	1040	CAGGGGCCCCACAGGTGCCCTGTGATGTGAGAGAGGCCCAAGCTCACCTCAGCTGCCACAC	1099
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Oy	1321	TCCACCCCAGAGCATATGGGCTGTATCACCAGACACACTCTGCCGCTGGGGGAACCTGC	1380
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Oy	1381	TGCCGACCCAGAGGGTGGGAGGCTGGGCTGTCTGCCAGTTTGCCCCAATGCTGTGTGCAG	1440
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Oy	1441	GATGCCACAGACTGTCTGCCCGGCTGTGCTACACCTTGCAAGTAGAGGCTGTGATTCTGGAG	1500
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Oy	1921	GGGAGTGGGGGCTCAATCTAAGGCCCTTCCCTGTGAGAAGGGGGTGTGAGGCAAAAGCC-	1979
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DEFINITION	H.sapiens mRNA for epithelin 1 and 2.		
ACCESSION	X62320.		
VERSION	X62320.1	GI:31192	
KEYWORDS	epithelial cell growth regulator; Epithelin 1; Epithelin 2; soluble protein.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Epithelin precursor encodes two proteins with opposing activities on epithelial cell growth		
JOURNAL	J. Biol. Chem. 267 (18), 13073-13078 (1992)		
MEDLINE	92317004		

PUBMED 161805
 REFERENCE 2 (bases 1 to 2152)
 AUTHORS Plozman, G.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-JAN-1991) G.D. Plozman, Oncogen, 3005 1st Avenue, Seattle, WA 98121, U S A
 COMMENT See also X6320-2.
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BASE COUNT 394 a 691 c 639 g 428 t
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Query Match 96.1%; Score 2014; DB 9; Length 2152;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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QY	1441	GATCGCCAGCAGCTGTGCTGCCGCGGTGGCTACACCTTGCAACGTGAAAGGCTGATCCTGCGAG	1500
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QY	1921	GGGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTACAAAGGGGTTGAGCAAAAGCC-	1979
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QY	1980	CATTACAGACTGCTCAATCCCTCCCGTTTCAGTGAGACCTGTGGCAGAGTGTCTTCCCT	2039
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LOCUS	AF055008	Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.	
DEFINITION	AF055008		
ACCESSION	AF055008.1	GI:3005729	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

FEATURES	source
JOURNAL	Anal. Biochem. 236 (1), 107-113 (1996)
MEDLINE	96207227
PUBMED	8619474
REFERENCE	2. (bases 1 to 2178)
AUTHORS	Yu, W., Anderson, B., Worley, R.C., Muzny, D.M., Ding, Y., Liu, W., Rocafrute, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.
TITLE	Large-scale concatenation cDNA sequencing
JOURNAL	Genome Res. 7 (4), 353-358 (1997)
MEDLINE	9110174
PUBMED	9110174
REFERENCE	3. (bases 1 to 2178)
AUTHORS	Yu, W. and Gibbs, R.A.
TITLE	Direct Submission
JOURNAL	Submitted (23-MAR-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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QY	121 GCGAGCTACAGCTGTGGCGTCCCTTTGGACAAATGGCCACCAACACTAGAGAGGAT 180
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QY	181 CTGGGTGGCCCTTCAGATGTGATGACCACTAGCTCTGGCGGCACTCTGTGATCTTTACC 240
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RESULT 5
AK000607

LOCUS
DEFINITION Homo sapiens cDNA FLJ20600 fis. clone KAT07521, highly similar to
ACCESSION AF050008 Homo sapiens clone 24720 epithelin 1 and 2 mRNA.
VERSION AK000607
KEYWORDS AK000607.1 GI:7020815
SOURCE oligo capping; fis (full insert sequence).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
REFERENCE
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE
JOURNAL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,
Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@iims.u-tokyo.ac.jp,
Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of

sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES

Location/Qualifiers

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epithelin 1 and 2 mRNA"

BASE COUNT 399 a 691 c 639 g 428 t

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Best Local Similarity 99.1%; Pred. No. 0;
Matches 2043; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

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DB 389 GGTAAACACACCTGG 448
QY 421 TCCAGCTGCTGTATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
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QY 541 CGGTGACATCAACCCAGGGGGAGCCACCCCTGGCAAAAGAGCTCCCTGGCCAGAGACT 600
DB 569 CGGTGACATCAACCCAGGGGGAGCCACCCCTGGCAAAAGAGCTCCCTGGCCAGAGACT 628
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QY 661 GATGGTTCTACCTGCTGTGAGCTGCCAGTGGAAATGTGGCTGGCTGGCTGGCT 720
DB 689 GATGGTTCTACCTGCTGTGAGCTGCCAGTGGAAATGTGGCTGGCTGGCTGGCT 748
QY 721 GCCACCTGCTGCTCCGATTCACCTGCACTGCTGCCGCCCAAGACACTGTGTGACTGATC 780

DB 749 GCCACTGCTGCTCCGATTCACCTGCACTGCTGCCGCCCAAGACACTGTGTGACTGATC 808
QY 781 CAGAGTAAGTGGCTTCCCAAGAGAGAGCTTACAGGAGCTTCCATCAATGAGCTGGG 840
DB 809 CAGAGTAAGTGGCTTCCCAAGAGAGAGCTTACAGGAGCTTCCATCAATGAGCTGGG 868
QY 841 CACACAGTGGGGAGTGAATGTGACATGAGTGGAGTGGCCAGATGGCTATACCTTC 900
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QY 901 TCCCTCTACAGTGG 960
DB 929 TCCCTCTACAGTGG 988
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QY 1141 ACCCTGTCACACTCAGCTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1200
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QY 1201 TGTCTGGACACACACACTGTGCCCCCAGCAGTACAGCTGTGTAGCTGAGGGGGAGTGT 1260
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QY 1321 TCCCAACCCAGAGATCGGTGTGTGACACAGACACAGCTGCCCCGGTGGGGGAACTTCG 1380
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QY 1381 TCCCGAGCAGAGTGGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1440
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QY 1441 GATCGCCAGACTGTGCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1500
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QY 1501 AAGGAAGTGGTCTGTGCCAGCTGCACTTCTGAGCCGATAGCCCTACAGTGGGGTGG 1560
DB 1529 AAGGAAGTGGTCTGTGCCAGCTGCACTTCTGAGCCGATAGCCCTACAGTGGGGTGG 1588
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DB 1589 AAGGAGTGGAGTGGGGAGAGACATTTCTGCATGATTAACAGACCTGTGCCAGAG 1648
QY 1621 AACCGAGAGGGTGG 1680
DB 1649 AACCGAGAGGGTGG 1708
QY 1681 CACTGCTGCTGTGGGCTTCCGCTGGCAGACAGAGGGATTAACAGAGTGTGGCAGAGAG 1740
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QY 1741 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCTTGAAGACAGCTGTGTGAGGAGACA 1800
DB 1769 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCTTGAAGACAGCTGTGTGAGGAGACA 1828
QY 1801 GTACTGAAGACTGTGACAGCCCTGGGAGCCCACTGGAGAGGGTCCCTGTGCTCAGGCTTC 1860

Db	1829	GNACGAGACATCTCAGCCCTCGGGACCCCACTCGAGAGGGTGCCCTGTCGACAGCCTC	1888
Qy	1861	CCTACACTCCCTCCCTAACCAAAATCTCTCCCTTGAGACCCATCTGAGCTCCCATACAT	1920
Db	1889	CTTACACCTCTCCCTTAACCAAAATCTCTCCCTTGAGACCCATCTGAGCTCCCATACAT	1948
Qy	1921	GGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAAGGGGTGAGGCAAAAGCC	1979
Db	1949	GGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAAGGGGTGAGGCAAAAGCC	2007
Qy	1980	CATTCAAGCTGCCATTCCTCCCTCCCTGTCAGTGAGACCTGTGGCAGGTGCTTTCCCT	2039
Db	2008	CATTCAAGCTGCCATTCCTCCCTCCCTGTCAGTGAGACCTGTGGCAGGTGCTTTCCCT	2067
Qy	2040	ATCCACAGGGGTGTGTGTGT 2061	
Db	2068	ATCCACAGGGGTGTGTGTGT 2089	
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LOCUS	AY124489	2124 bp	mRNA linear PRI 14-AUG-2002
DEFINITION	Homo sapiens PC cell-derived growth factor (GRN) mRNA, complete cds.		
ACCESSION	AY124489		
VERSION	AY124489.1	GI:22252939	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2124)		
AUTHORS	Lu, R., Tian, C. and Serrero, G.		
TITLE	PCGF sequence from lambda phage human Jurkat T cell cDNA library (Clontech)		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2124)		
AUTHORS	Lu, R., Tian, C. and Serrero, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUN-2002) Pharmaceutical Sciences, University of Maryland School of Pharmacy, 20 N. Pine St., Baltimore, MD 21201, USA		
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	/cell_line="Jurkat"		
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	/protein_id="AAMG4026.1"		
	/db_xref="GI:22252940"		
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BASE COUNT	377 a 683 c 635 g 429 t		
ORIGIN			
Query Match	95.4%	Score 1998:	DB 9; Length 2124;
Best Local Similarity	98.9%	Pred. No. 0;	
Matches 2045; Conservative	0;	Mismatches 15; Indels 8; Gaps 3;	

QY	1	CCGAGGAGACAAATGTTGGACCTCGTGAGCTGGGTGGCCCTTAACAGACAGGGCTGGTGGCT	60
Db	7	CGAGGAGACAAATGTTGGACCTCGTGAGCTGGGTGGCCCTTAACAGACAGGGCTGGTGGCT	66
QY	61	GGAACGGGGGCCAGATGTGCTAGTTCTGCGCCCTGTGGCTCTGCTGGCTGGAGCCCGGAGGA	120
Db	67	GGAACGGGGGCCAGATGTGCTAGTTCTGCGCCCTGTGGCTCTGCTGGCTGGAGCCCGGAGGA	126
QY	121	GCCAGCTACAGCTGTGCGGTCCCCCTTCTTGAGCAATATGGCCCAACAACACTAGCAGGCAT	180
Db	127	GCCAGCTACAGCTGTGCGGTCCCCCTTCTTGAGCAATATGGCCCAACAACACTAGCAGGCAT	186
QY	181	CTGGGTGGCCCCCGGAGTTGATATGGCCACTGTGCTGCGGGGACATCCGATCTTTTACC	240
Db	187	CTGGGTGGCCCCCGGAGTTGATATGGCCACTGTGCTGCGGGGACATCTGCACTTTTACC	246
QY	241	GTCACAGGACTTCAGATTGCTCCGCCCTTCCAGAGAGCCGTGGAGTGGCGGGATGGCCAT	300
Db	247	GTCACAGGACTTCAGATTGCTCCGCCCTTCCAGAGAGCCGTGGAGTGGCGGGATGGCCAT	306
QY	301	CACATGCTGCCACAGGGGCTTCCACTGCACTGCAATGCAGAGGGGCATCTGCTTCCAAAGATCA	360
Db	307	CACATGCTGCCACAGGGGCTTCCACTGCAATGCAGAGGGGCATCTGCTTCCAAAGATCA	366
QY	361	GGTAAACAATCCGTTGGGTGGCATTCAGATGCGCCGATATGATTTGAAATGGCCCGGACTTC	420
Db	367	GGTAAACAATCCGTTGGGTGGCATTCAGATGCGCCGATATGATTTGAAATGGCCCGGACTTC	426
QY	421	TCCACGTGCTGTATTATGATGATGAGCTCTCGGGGGTGTGCCCCATGCCCGAGGCTTCC	480
Db	427	TCCACGTGCTGTATTATGATGATGAGCTCTCGGGGGTGTGCCCCATGCCCGAGGCTTCC	486
QY	481	TGCTGTAAACAGAGGTGGCACTGCTGTCCGCAAGGTGCTTCTGCGACCTGGTTACACC	540
Db	487	TGCTGTAAACAGAGGTGGCACTGCTGTCCGCAAGGTGCTTCTGCGACCTGGTTACACC	546
QY	541	CGCTGCATACACACCCAGCGGACCCAGCCCGCGGCAAAACATCCCTGCCAGAGGACT	600
Db	547	CGCTGCATACACACCCAGCGGACCCAGCCCGCGGCAAAACATCCCTGCCAGAGGACT	606
QY	601	AACAGGGCAGTGGCCCTTGTGTCAGCTGCGTATGTGTCCGGACGACGGTCCCGGTGCCCT	660
Db	607	AACAGGGCAGTGGCCCTTGTGTCAGCTGCGTATGTGTGTCCGGACGACGGTCCCGGTGCCCT	666
QY	661	GATGGTCTTACCTGTGTGTAGTGTGCCCAATGGGTATGGTGTGCTGCCCAATGCCCAAC	720
Db	667	GATGGTCTTACCTGTGTGTGTAGTGTGCCCAATGGGTATGGTGTGCTGCCCAATGCCCAAC	726
QY	721	GCCACCTGCTGCTCCGATACCTGCACTGCACTGTCGCCCAAGACACTGTGTGATGACTGATC	780
Db	727	GCCACCTGCTGCTCCGATACCTGCACTGCACTGTCGCCCAAGACACTGTGTGATGACTGATC	786
QY	781	CAGATGATGTGCTCTTCCAGAGGAAGCTTACCAGGACCTTCTCACTTAAGCTGCTGGC	840
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QY	841	CACACATGSGGCGATGTGAATGTGACATGTGAGGTAGCTGCCAGATGGCTATATCTGC	900
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QY	901	TGCGCTGTACAGTGTGGGGGCTGGGGCTGCTCCCTTTTACCAAGAGCTGTGTGCTGTAG	960
Db	907	TGCGCTGTACAGTGTGGGGGCTGGGGCTGCTCCCTTTTACCAAGAGCTGTGTGCTGTAG	966
QY	961	GACCACATACACTGTGTGTCCCGGGGTTTACGTGTGACACGACAGAGGGTACCTGTGAA	1020
Db	967	GACCACATACACTGTGTGTCCCGGGGTTTACGTGTGACACAGAGGGTACCTGTGAA	1026
QY	1021	CAGGGGCCCCACAGGTGCCCTGTGATGTGGAAGAGCCCCAGCTCAACCTCAGCTGCGACAC	1080
Db	1027	CAGGGGCCCCACAGGTGCCCTGTGATGTGGAAGAGCCCCAGCTCAACCTCAGCTGCGACAC	1086

QY 1081 CCACAAAGCTTGAAGAGATGTCCTGTCGTGATATGTCAGACAGCTGTCCTCTCCGAT 1140
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 DB 1147 ACCTGCTGCCAATCAACGTCTGGGAGATGGGGCTGCTGTCCAAATCCAGAGCTGTGTC 1206
 QY 1201 TGTCTGGACACAGACACTGTCGCCCCCAGAGATACAGTGTATAGCTGAGGGGAGTGT 1260
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 QY 1381 TCCCGAGCCAGAGGTGGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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 DB 1447 GATGCGCAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
 QY 1501 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
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 DB 1507 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1566
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 DB 1567 AAGGAGCTGAGTGTGGGGAAGAGACATCTGTCATATTAACACAGACTGCTGCTGCTGCTG 1626
 QY 1621 AACCGACAGGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
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 DB 1627 AACCGACAGGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686
 QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
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 DB 1687 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746
 QY 1741 GCCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCTTGAGACAGCTGCTGCTGCTGCTGCTG 1794
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 DB 1747 GCCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCTTGAGACAGCTGCTGCTGCTGCTG 1806
 QY 1795 GGGACAGTACTGAAGACTGTGACAGCCCTGAGGAGCCCACTGAGAGGGTGCCTGCTGCTG 1854
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 DB 1807 GGGACAGTACTGAAGACTGTGACAGCCCTGAGGAGCCCACTGAGAGGGTGCCTGCTGCTG 1866
 QY 1855 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1914
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 DB 1867 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1926
 QY 1915 CACCATGGAGTGTGGGCTCAATCTTAAGCCCTTCCCTGTCAGAAAGGGGCTTGTAGGCA 1974
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 DB 1927 CACCATGGAGTGTGGGCTCAATCTTAAG -CCTTCCCTGTCAGAAAGGGGCTTGTAGGCA 1985
 QY 1975 AAGCC-CATTACAAGTGCATCCCTCCCGTTTCAAGTGAAGCCCTGTGGCAGAGTGT 2033
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 DB 1986 AAGCCCAATTTACAGAGTGCATCCCTCCCGTTTCAAGTGAAGCCCTGTGGCAGAGTGT 2045
 QY 2034 TTCCCTATCCACAGGGGTGTTGTGT 2061
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 DB 2046 TTCCCTATCCACAGGGGTGTTGTGT 2073

ACCESSION AR079655
 VERSION AR079655.1 GI:10006396
 KEYWORDS
 SOURCE
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 1779)
 TITLE Shoyab,M. and Plowman,G.D.
 JOURNAL DNA encoding epithelins
 FEATURES Patent: US 5965723-A 3 12-0CT-1999;
 Location/Qualifiers
 source 1..1779
 BASE COUNT 304 a 578 c 547 g 350 t
 ORIGIN
 Query Match 83.8%; Score 1756.6; DB 6; Length 1779;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1765; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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 QY 73 CCAGATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
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 DB 61 CCAGATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 133 TGTCTGCGTCCCTTCTGTGGACAAATGGCCCAACACTAGACAGCATGTGGTGGCCCC 192
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 DB 121 TGTCTGCGTCCCTTCTGTGGACAAATGGCCCAACACTAGACAGCATGTGGTGGCCCC 180
 QY 193 TSCAGATGTGATGCCACACTGCTGCTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
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 DB 181 TSCAGATGTGATGCCACACTGCTGCTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 233 TCCAGTGTGCTGCCCTTCCACAGAGCCGTGGCATGGCGGGAATGGCCATCACTGCTGCCCA 312
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 DB 241 TCCAGTGTGCTGCCCTTCCACAGAGCCGTGGCATGGCGGGAATGGCCATCACTGCTGCCCA 300
 QY 313 CGGGGCTTCCACTGCAAGTGCACACAGGGGCAATCTGCTTCCAAAGATCAAGTAACACTGC 372
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 DB 301 CGGGGCTTCCACTGCAAGTGCACACAGGGGCAATCTGCTTCCAAAGATCAAGTAACACTGC 360
 QY 373 GTGGGTGCATCCAGTGCCTGATAGTCAAGTGAATGGCCGAGCTTTCACAGTGTGCTG 432
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 DB 361 GTGGGTGCATCCAGTGCCTGATAGTCAAGTGAATGGCCGAGCTTTCACAGTGTGCTGCTG 420
 QY 433 GTTATGTCGATGAGTCTGCTGGGGGTGCTGCCCATGCCAGAGCTTCTGCTGTGAAGAC 492
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 DB 421 GTTATGTCGATGAGTCTGCTGGGGGTGCTGCCCATGCCAGAGCTTCTGCTGTGAAGAC 480
 QY 493 AAGGTGCATGCTGTGTCGCGACAGGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
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 DB 481 AAGGTGCATGCTGTGTCGCGACAGGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 553 CCCAGGGGACACACCCCTTGGCAAAAGAGTCCCTGCGCAGAGGACTTAACAGGGGAGTG 612
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 DB 541 CCCAGGGGACACACCCCTTGGCAAAAGAGTCCCTGCGCAGAGGACTTAACAGGGGAGTG 600
 QY 613 GCTTGTCCAGTGGGTGATGTGTCGAGAGCAGAGGTGCCGGTGCCTGATGGTTTCTAC 672
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 QY 673 TGTCTGAGCTGCCAGTGGGAAGTATGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
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 DB 661 TGTCTGAGCTGCCAGTGGGAAGTATGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 733 TCCGATCACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
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 DB 721 TCCGATCACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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RESULT 8
 LOCUS AR079655 1779 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 3 from patent US 5965723.

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D	841	GATGTGAATGTGACATGAGAGTGAAGCTGCGCAGATGGCTATACCTGCTGCCGTCTACAG	900
Q	913	TGCGGGGCGCTGGGGGCTGCTGCTTTACCCAGAGCTGTGTGTGTGAGAGCACATACAC	972
D	901	TGCGGGGCGCTGGGGGCTGCTGCTTTACCCAGAGCTGTGTGTGTGAGAGCACATACAC	960
Q	973	TGCTGTCCCGGGGGTTTACGTGTGACACGCGAAGAGGTACCTGTGAACAGGGCCCCAC	1032
D	961	TGCTGTCCCGGGGGTTTACGTGTGACACGCGAAGAGGTACCTGTGAACAGGGCCCCAC	1020
Q	1033	CAGGTGCCCTGGATGGAAAGGCCCCACCTCACTCAGCTGCGCAGACCCAAACGCTTG	1092
D	1021	CAGGTGCCCTGGATGGAAAGGCCCCACCTCACTCAGCTGCGCAGACCCAAACGCTTG	1080
Q	1093	AAGAGAGATGTCCCTGTGATTAATGTACAGAGCTTCCCTCCGATTAACGTGTGCACA	1152
D	1081	AAGAGAGATGTCCCTGTGATTAATGTACAGAGCTTCCCTCCGATTAACGTGTGCACA	1140
Q	1153	CTCAGCTCTGGGGAATGGGGGCTGCTGTCCATCCAGAGGCTGTCTGCTGTGAGACAC	1212
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Q	1273	GAGATCGTGGCTGGACTGGAGAAAGATGCCCTGCGCGCGGTTCTTATCCACCCACA	1332
D	1261	GAGATCGTGGCTGGACTGGAGAAAGATGCCCTGCGCGCGGTTCTTATCCACCCACA	1320
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Q	1393	GGTGGAGCTGGGCGCTGTGTCACAGTGTGCCCTCTGTGTGTGCGAGAGATGCCAGCAC	1452
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Q	1453	TGCTGCCGCGGTGGGTAACTTGCACCTGAAAGCTCGATCTCGGAGAAAGAAATGGTC	1512
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D	1561	TGTGGGGAAGACACTTGTGCCATGTATTAACAGACCTCTGCGAGACACCGACAGGCG	1620
Q	1633	TGGGCTCTCTGCCCTACGCCAGAGGCGCTGTGTGTGTGATCGGCGCACATGCGTCT	1692
D	1621	TGGGCTCTCTGCCCTACGCCAGAGGCGCTGTGTGTGTGATCGGCGCACATGCGTCT	1680
Q	1693	GCTGGCTCCGCTGCGACGACGAGGGGTACCAAGTGTGTGCGAGGAGGCGCCGCGCTGG	1752
D	1681	GCTGGCTCCGCTGCGACGACGAGGGGTACCAAGTGTGTGCGAGGAGGCGCCGCGCTGG	1740
Q	1753	GACGCGCCTTTGAGGAGACCCAGCCTTTGAGACAGCTGCTG	1791
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RESULT 9			
LOCUS	111830		
DEFINITION	Sequence 3 from Patent US 5416192.		
ACCESSION	111830		
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		linear	PAT 26-JUL-1995

VERSION	KEYWORDS	GI:909273
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 1779)	
TITLE	Shoyab,M. and Plozman,G.D.	
JOURNAL	Epithelins: novel cysteine-rich growth modulating proteins	
FEATURES	Patent: US 5416192-A 3 16-MAY-1995;	
Source	Location/Qualifiers	
	1..1779	
BASE COUNT	304 a 578 c 547 g 350 t	
ORIGIN		
Query Match	83.8%;	Score 1756.6;
Best Local Similarity	99.2%;	Pred. No. 0;
Matches 1765;	Conservative 0;	Mismatches 14; Indels 0; Gaps 0;
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1	ATGTGACCCCTGGTGTAGCTGGGGTGGCCCTTAAACAGAGGGGCTGTGGCTGGAGACGGCGTGC	60
73	CCAGATGTGCAATGTTCGCTGTGGCTGTGGCTGTGGAGCCCGGAGGAGCCAGCTACAGC	132
61	CCAGATGTGCAATGTTCGCTGTGGCTGTGGCTGTGGAGCCCGGAGGAGCCAGCTACAGC	120
133	TGCTCCGCGTCCCTCTGTGGACAAATGGCCCAACACATGAGGAGCATCTGGGTGGCCCC	192
121	TGCTCCGCGTCCCTCTGTGGACAAATGGCCCAACACATGAGGAGCATCTGGGTGGCCCC	180
193	TGCCAGGTGTGATGCCCACACTGTCTCCCGGCCACTCTGTGATCTTTACGGCTCCAGGACT	252
181	TGCCAGGTGTGATGCCCACACTGTCTCCCGGCCACTCTGTGATCTTTACGGCTCCAGGACT	240
253	TCCAGTTGCTGCGCCCTTCCCAAGAGGCCGCTGGGATGCGGGATGGGCATCTACTGCTGCCA	312
241	TCCAGTTGCTGCGCCCTTCCCAAGAGGCCGCTGGGATGCGGGATGGGCATCTACTGCTGCCA	300
313	CGGGGCTTCCACTGCAGTGCAGACAGCGGGGATCTCTTCCAAAGATCAGGTAAACAATCC	372
301	CGGGGCTTCCACTGCAGTGCAGACAGCGGGGATCTCTTCCAAAGATCAGGTAAACAATCC	360
373	GTGGTGCCATTCAGTGGCCCTGTATGTGTCAGTTGCAATGCGCGGACTTCTCCACGTGCTGT	432
361	GTGGTGCCATTCAGTGGCCCTGTATGTGTCAGTTGCAATGCGCGGACTTCTCCACGTGCTGT	420
433	GTATGTCGATAGGCTGCTCGGGGGGAGTGCCTCCATAGGCCCAAGGCTTCTCGCTGTAAAGC	492
421	GTATGTCGATAGGCTGCTCGGGGGGAGTGCCTCCATAGGCCCAAGGCTTCTCGCTGTAAAGC	480
493	AGGGTGCACGTGTCGCGCACAGGTGCTCTTTCGACACGTGTTACACACCGCGTGCATACA	552
481	AGGGTGCACGTGTCGCGCACAGGTGCTCTTTCGACACGTGTTACACACCGCGTGCATACA	540
553	CCCAAGGGGACACCCCTTGGCAAAAGAGTCCCTGGCCAGAGAGCTTAACAGGGGACGTG	612
541	CCCAAGGGGACACCCCTTGGCAAAAGAGTCCCTGGCCAGAGAGCTTAACAGGGGACGTG	600
613	GCCCTGTCCAGCTGGTATGTGTCCGAGACGACGGTCCCGGTGGCCAGATGGTCTTACC	672
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673	TGCTGTGAGCTGCCAGTGGGAGTATGAGTGTGCTGCCCAATGCCCCAACGCCACTGTGTC	732
661	TGCTGTGAGCTGCCAGTGGGAGTATGAGTGTGCTGCCCAATGCCCCAACGCCACTGTGTC	720
733	TCCGATTCACCTGCATCTGTGGCCCCCAACACATGTGTGACCTGTATCCAGAGTAAGTGC	792
721	TCCGATTCACCTGCATCTGTGGCCCCCAACACATGTGTGACCTGTATCCAGAGTAAGTGC	780
793	CTTCTCAAGGAGAACGTACACAGGAGCTCTCTCAATAGCTGCTGCGCACACATGGGCG	852

D	781	CTCTCAAGGAAAGACGTACACAGGACCTCTCACTAAGCTGCTGGGACACAGTGGGG	840
Q	853	GATGTGAAATGTGACATGGAGGTGAGCTGCCCCAGATGGCTATACCTGCTGCCGTGTACAG	912
D	841	GATGTGAAATGTGACATGGAGGTGAGCTGCCCCAGATGGCTATACCTGCTGCCGTGTACAG	900
Q	913	TGGGGGGCTGGGGGTGTGGCTTTTACCGAGGTGTGTGTGTGAGAGACCACTATAC	972
D	901	TGGGGGGCTGGGGGTGTGGCTTTTACCGAGGTGTGTGTGTGAGAGACCACTATAC	960
Q	973	TGCTGTCCCGGGGGGTTTACGTGTGACACGAGAAAGGGTACTCTGTGAACAGGGGCCAC	1032
D	961	TGCTGTCCCGGGGGGTTTACGTGTGACACGAGAAAGGGTACTCTGTGAACAGGGGCCAC	1020
Q	1033	CAGGTGCCCTGGATGTGACAAAGGCCCACTCACTCAAGCTGCGACAGACCCACAGCCTTG	1092
D	1021	CAGGTGCCCTGGATGTGACAAAGGCCCACTCACTCAAGCTGCGACAGACCCACAGCCTTG	1080
Q	1093	AAGAGAGATGTCCCTGTGATTAATGTACAGACGCTCCCTCTCCGATACCTGCTGCCAA	1152
D	1081	AAGAGAGATGTCCCTGTGATTAATGTACAGACGCTCCCTCTCCGATACCTGCTGCCAA	1140
Q	1153	CTCACGTCTGGGGAGTGGGGGCTGTCTCAATCCAGAGGCTGTCTGTCTGGAGCAC	1212
D	1141	CTCACGTCTGGGGAGTGGGGGCTGTCTCAATCCAGAGGCTGTCTGTCTGGAGCAC	1200
Q	1213	CAGCACTCTCTGCCCCCAGCATACACGTGTGTAGTGTGAGGGGCACTGTACGAGAGAAC	1272
D	1201	CAGCACTCTCTGCCCCCAGCATACACGTGTGTAGTGTGAGGGGCACTGTACGAGAGAAC	1260
Q	1273	GAGATCGTGGCTGTGACTGTGAGAAAGATGGCTGGCCCGCGGGTTCCTTATCCCACTCCAGA	1332
D	1261	GAGATCGTGGCTGTGACTGTGAGAAAGATGGCTGGCCCGCGGGTTCCTTATCCCACTCCAGA	1320
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D	1321	GACATCGGCTGTGACACACACACAGCTGCCCCGGTGGGGGCGAACTGCTGCCAGCCAG	1380
Q	1393	GGTGGGACCTGGGCTGCTGCTGCACATGGTGGCCCATGCTGTGTGTGGGAGATGCCAGCAC	1452
D	1381	GGTGGGACCTGGGCTGCTGCTGCACATGGTGGCCCATGCTGTGTGTGGGAGATGCCAGCAC	1440
Q	1453	TGCTGCCCGGGTGTGTACACCTGTCAACGTGAAGGCTCATCTGTGAGAGAAAGATGTGTC	1512
D	1441	TGCTGCCCGGGTGTGTACACCTGTCAACGTGAAGGCTCATCTGTGAGAGAAAGATGTGTC	1500
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Q	1573	TGTGGGGAAGGACACTTGTGGCATATTAACAGACACTGTGCCCGAGACAAACCGAAGGGC	1632
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D	1621	TGGGCTACTGTCTCCCTACAGCCAGGGGCTGTGTGTGTGATCGAGCGCACTGTCTCT	1680
Q	1693	GCTGGCTTCCTGCTGCGCACAGCGAGGGGTACCAAGTGTGTTCGCGAGGAGGCCCGCGCTGG	1752
D	1681	GCTGGCTTCCTGCTGCGCACAGCGAGGGGTACCAAGTGTGTTCGCGAGGAGGCCCGCGCTGG	1740
Q	1753	GACGCCCTTTGAGGAGACCAACACTTTGAGACAGCTGCTG	1791
D	1741	GACGCCCTTTGAGGAGACCAACACTTTGAGACAGCTGCTG	1779

RESULT 10	AK023348	LOCUS	DEFINITION	ACCESSTION
	AK023348	1630 bp	mRNA	linear
				PRI 01-AUG-2002
				Homo sapiens cDNA FLJ13286 f1s, clone OVAR1001154, highly similar
				to Homo sapiens clone 24720 epithelin 1 and 2 mRNA.
				AK023348

VERSION	AK023348.1	GI:10435243
KEYWORDS	Oligo capping, fis (full insert sequence).	
SOURCE	Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_id:OVARC1 clone:OVARC1001154.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE AUTHORS	1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Shiratori,A., Sudo,H., Magatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murekami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuno,Y., Ninomiya,K. and Iwayanagi,T. NEDO human cDNA sequencing project	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 1630)	
REFERENCE	Isogai,T. and Otsuki,T.	
AUTHORS	Direct Submission	
TITLE	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 229-0012, Japan (E-mail:genomics@hli.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	
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	Query Match	
	Best Local Similarity 84.9%; Pred. No. 7.9e-268;	
	Matches 1574; Conservative 0; Mismatches 18; Indels 262; Gaps 3;	
QY	209	ACTGCTGTCCGGCCACTCTGTCATCTTTACCGTCTCAGGACCTTCAGTTGCTGCCCT 268
DB	1	ACTGCTGTCCGGCCACTCTGTCATCTTTACCGTCTCCAGGGACCTTCAGTTGCTGCCCT 60
QY	269	TCCCAAGAGCCGTGGCATCGCGGGGATGGCCATCATGTGTCGCCACGCGGCTTCACCTGCA 328
DB	61	TCCCAAGAGCCGTGGCATCGCGGGGATGGCCATCATGTGTCGCCACGCGGCTTCACCTGCA 120
QY	329	GTGCAGAGCGGCGATCCCTGCTTCCAAATATCAGGTAAACATCCGTGGGTGCATTCACGT 388
DB	121	GTGCAGAGCGGCGATCCCTGCTTCCAAATATCAGGTAAACATCCGTGGGTGCATTCACGT 180

QY 389 GCCCTATATGCTGTAATGCTGCGGACTTCTCAGCTGTGTATGATGATGCT 448
 DB 181 GCGCTATATGCTAGTTGTAATGCTGCGGACTTCTCAGCTGTGTATGATGATGCT 240
 QY 449 CCGGGGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 508
 DB 241 CCGGGGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
 QY 509 CCGACGGTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
 DB 296 ----- 295
 QY 569 CCGTGGCAAGAGCTCCCTGCCAGAGACTAAGGCGAGTGGCTTGTCCAGCTGG 628
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 QY 929 GGTGCGCTTTTCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 988
 DB 461 GGTGCGCTTTTCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 520
 QY 989 TTACGCTGTGACAGCGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1048
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 QY 1049 AGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1108
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 QY 1109 GTGATATGTGTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1168
 DB 641 GTGATATGTGTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 700
 QY 1169 GGGGCTGT 1228
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 QY 1289 TGGAGATATGCTGT 1348
 DB 821 TGGAGATATGCTGT 880
 QY 1349 AGCAGCAGGCTGT 1408
 DB 881 AGCAGCAGGCTGT 940
 QY 1409 GCTGCGAGT 1468
 DB 941 GCTGCGAGT 1000
 QY 1469 ACACCTGCAAGGTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1528

DB 1001 AACACGTGCAAGCTGGAAGGCTGCATCTGCGAGAGAAAGTGTCTCTGCCAGCTGCCA 1060
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 DB 1421 CCTGAGCCCATTTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1479
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 DB 1480 TCCCTGTGAGAGGCGGT 1539
 QY 2008 TCAGTGAACCTGT 2061
 DB 1540 TCAGTGAACCTGT 1593

RESULT 11
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 LOCUS 2153 bp mRNA linear ROD 26-AUG-1992
 DEFINITION R. norvegicus mRNA for epithelin 1 and 2.
 ACCESSION X63322
 VERSION X63322.1 GI:56108
 KEYWORDS epithelial cell growth regulator; Epithelin 1; Epithelin 2; soluble protein.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 2153)
 Plozman,G.D., Green,J.M., Neubauer,M.G., Buckley,S.D., McDonald,V.L., Todaro,G.J. and Shoyab,M.
 The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth
 J. Biol. Chem. 267 (18), 13073-13078 (1992)
 JOURNAL 92317004
 MEDLINE 1618805
 PUBMED 2 (bases 1 to 2153)
 REFERENCE Plozman,G.D.
 AUTHORS Plozman,G.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-JAN-1991) G.D. Plozman, Oncogen, 3005 1st Avenue, Seattle, WA 98121, U S A
 COMMENT See also X63320-2.
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RESULT 12
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LOCUS RatGABEL12A 2113 bp mRNA linear ROD 23-MAR-1994
DEFINITION RatGABEL12A 2113 bp mRNA linear ROD 23-MAR-1994
ACCESSION M97750
VERSION M97750.1 GI:204223
KEYWORDS epithelin; granuln.
SOURCE RatGABEL12A 2113 bp mRNA linear ROD 23-MAR-1994
ORGANISM Rattus norvegicus (Strain Sprague-Dawley) (library: lambda-gt11)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2113)
REFERENCE Bhandari,V., Glaid,A. and Bateman,A.
AUTHORS The complementary deoxyribonucleic acid sequence, tissue
TITLE distribution, and cellular localization of the rat granuln
precursor
JOURNAL Endocrinology 133 (6), 2682-2689 (1993)
MEDLINE 94062640
PUBMED 8243292
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JOURNAL Endocrinology 133 (6), 2682-2689 (1993)
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Best Local Similarity 76.9%; Pred. No. 1.2e-257;
Matches 1591; Conservative 0; Mismatches 454; Indels 24; Gaps 7;
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DB 70 AGTGCCAGATGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
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ORIGIN	

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Best Local	Similarity	75.8%	Pred. No. 2.2e-255:		
Matches 1574:	Conservative	0:	Mismatches 483:	Indels	Gaps
OY	1	CGCAGCGACCCATGTGACCCCTGGTGAAGTGGGTGAGCCCTTAACAGAGGGCTGGTGGCT	60		
Db	13	CGCAGGCGACCATATGGGGTCTGTATGAGCTGGCTGGCCCTTCGCGGAGGGCTGGTAGCC	72		
OY	61	GGAAAGCGAGTGGCCGAGATGATGATTCAGCCCTGGGGCTGGTGGCTGGAGCCGGAGGA	120		
Db	73	GGAAACAGATGTCCAGATGGGAGATTCTGGCCCTGTGGCTGTGGCTTGGACAGGAGGA	132		
OY	121	GCCAGCTACAGCTGTGTCGGTCCCTTCCTTGGACAAGTGGCCACAACTAGCAGGAGAT	180		
Db	133	GCCAACTACACTGTGCTTAACCCCTTCTTGGGACATGGCTAGAAATACGAGCATCAT	192		
OY	181	CTGGGTGGCCCCCTGGCAGATTGATGCCACAGTCTGTGGCGGCACTCCGATCTTTACC	240		
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OY	241	GTTCTAGGAGACTTCAGTTGCTGCCCTTCCAGAGGCCGTGGCATGGCGGGATGGCCAT	300		
Db	253	GTGTTGGAGACTTCAGTGTGCTGCCCTTCTTAAGGAGTGTGTGTTGGTGAATGGCTAC	312		
OY	301	CACGCTCCGCCAGGGGGTTCCACTGCAAGTGCAGACGGGGCATCTGTTCCAAAGATCA	360		
Db	313	CACGCTCCGCCAGGGGGTTCCACTGTAAGTGCAGATGGGAAATCTGTTCCAGATGTCA	372		
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Db	373	G---ATAACCCCTTGGGTGCTGTCCAGTGTCTCTGGGAGCCATTGGAATGTCTACTCT	429		
OY	421	TTCCAGTCTCTGTTATGATGGATGGCTCTCGGGGGTCTGCCCATGCCCCAGGCTTC	480		
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OY	481	TTGGTGAAGACAGGGTGCATCGTGTGCGCAGAGTGCCTTCTGGACCGGTGCACAC	540
Db	480	TGCTGTGAAGACAAGTGCATGTGTGTCCCAATGGGGCTCTGTACCTGGTTACACA	549
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OY	601	AACAGGCGATGGCCCTTGTCAGCTGGGTCAATGTTCGGAGCGACAGTCCGGTCCCT	660
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OY	661	GATGGTTCTACTCTCTGAGAGCTGCCAGTGGGAAGTATGGCTGGCCCAATGGCCAAC	720
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OY	721	GCCACTGTCTCTCCGATTCACCTGCATCGTGGCCCCCAAGACACTGTGTGACCTGATC	780
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Db	847	TACCCAGTGAAGAGGTGAAGTGGCATGAGAGTGGTGGCTTCAAGAAATATATCTGC	906
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Db	1087	CCACAGATCTTGAAGAGTGAATACACTTGTGTGATGACTTCACTAAGTGTCTTACAAACAT	1144
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OY	1261	CAGGAGGAACGAGATTCGTGGCTGGAGCTGGAGAAAGTGGCTGCCGCGCGGTTCCCTTA	1320
Db	1267	CAGAGGGAGACACAATGTGTGTGCTGTGGCTTGGAGAAATACTTCTCCCGCCAGAACCTCG	1326
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OY	1441	GATGCCAGACATCTGTCCCGGCTGGGTAACTGTGAAGTGAAGGCTGGAATCTGTGCGAG	1500
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QY	1561	AAAGACGTGAGATGTGGGGGAAAGACACTTCTTGCCATGATTAACAGACACTGCTGCCGAAC	1620
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QY	1621	AACCCACAGAGGCGTGGGGCCGTGGCTGATCCCTCAAGGCCACGGGCGTCTGTGTGCTGATCGGGGC	1680
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Db	1681	CACGTGTCTCCCGGTGGCTTCCACTGTTCAGCAGCAGGGGAACCAATGTTTGTGGAAGAAG	1740
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QY	1801	GTACTGAA-----GACTCTGACAGCCCTCGGGAACCCACTGCGAGGGTGCCTCTGCTC	1853
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QY	1913	ATCACACTGGAGAGTGGGGCCTCAATCTAAGGCCCTTCCCTGTCTGAAAGGGGGTTGAGC	1972
Db	1921	ATCACCAATGGGAGGTGGAGGACCTCAAAACTTCTTTTATGGAAGAAGAGCTGTGGC	1980
QY	1973	AAAAGCCCATTTCAACAGCTGCGCATGCCCTCCCGCTTCAAGTGGAGACCTGTGGCCAGTGCT	2032
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VERSION	ARI175447.1	GI:17916746	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2137)		
AUTHORS	Serrero,G.		
TITLE	88Da tumorigenic growth factor and antagonists		
JOURNAL	Patent: US 6309826-A 1 30-OCT-2001;		
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Query Match	57.3%;	Score 1200;	DB 6;	Length 2137;
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Db	181	TGGCTCTGCGACAGACCATTAGCCACTGTCCTCTGTGGATATCTCTGTCTTCTCATCTGTTC	240
QY	246	AGGAGCTTCAGTTGGTGGGCCCTTCCACAGAGGCCCTGGCAGTCGGGGGTGGCCATCACTG	305
Db	241	TGGGACTTCCAGCTGCTGCCCCCTTCTTAAGGGTGTGCTCTGTGGTATGGCTACCACTG	300
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Job time : 5408 secs
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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 13:23:23 ; Search time 168 Seconds
(without alignments)
7003.777 Million cell updates/sec

Title: US-08-991-862-16

Perfect score: 2095
Sequence: 1 CGCAGGCGAGCAGCAGTGTGAC.....ATAAGTTGTCACCTTCT 2095

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2095	100.0	2095	9	US-09-824-647-16	Sequence 16, Appl
2	2095	100.0	2095	10	US-09-813-156-16	Sequence 16, Appl
3	2095	100.0	2095	10	US-09-824-807-16	Sequence 16, Appl
4	2014	96.1	2432	10	US-09-925-301-574	Sequence 574, Appl
5	1200	57.3	2137	9	US-09-824-647-1	Sequence 1, Appl
6	1200	57.3	2137	10	US-09-813-156-1	Sequence 1, Appl
7	1200	57.3	2137	10	US-09-824-807-1	Sequence 1, Appl
8	483.8	23.1	561	10	US-09-884-441-89	Sequence 89, Appl
9	381.2	18.2	561	10	US-09-884-441-90	Sequence 90, Appl
10	270.4	12.9	400	10	US-09-960-352-6772	Sequence 6772, Ap
11	236.4	11.3	398	10	US-09-960-352-9598	Sequence 9598, Ap
12	228.8	10.9	233	10	US-09-864-761-27557	Sequence 27557, A
13	197.8	9.4	336	9	US-10-015-219-783	Sequence 783, App
14	197.8	9.4	336	10	US-09-777-564-783	Sequence 783, App
15	193.6	9.3	390	10	US-09-864-761-10921	Sequence 10921, A
16	139	6.6	561	10	US-09-884-441-90	Sequence 90, Appl
17	131.2	6.3	260	10	US-09-833-381-1292	Sequence 1292, Ap
18	118.6	5.7	760	10	US-09-910-943-148	Sequence 148, App
19	107.6	5.1	250	10	US-09-867-701-10072	Sequence 10072, A

C	20	55.6	2.7	108	10	US-09-867-701-10039	Sequence 10039, A
	21	38	1.8	99014	9	US-09-880-107-3428	Sequence 3428, Ap
	22	37.4	1.8	1816	10	US-09-974-298-18	Sequence 18, Appl
C	23	37.2	1.8	2108	10	US-09-962-832-225	Sequence 225, App
	24	36.6	1.7	310	10	US-09-923-876-3623	Sequence 3623, Ap
	25	36.6	1.7	1721	10	US-09-864-864-280	Sequence 280, App
	26	36.6	1.7	1721	10	US-09-967-768A-224	Sequence 224, App
	27	36	1.7	476	10	US-09-864-761-14282	Sequence 14282, A
	28	36	1.7	2009	9	US-10-047-542-54	Sequence 54, Appl
	29	36	1.7	2770	12	US-10-027-075-29	Sequence 29, Appl
	30	35.8	1.7	1171	9	US-09-945-182-25	Sequence 25, Appl
	31	35.8	1.7	8269	10	US-09-764-887-452	Sequence 452, App
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	33	35.8	1.7	8269	10	US-09-764-853-879	Sequence 879, App
C	34	35.8	1.7	88421	9	US-09-976-059-1	Sequence 1, Appl
	35	35.6	1.7	1804	10	US-09-964-824A-573	Sequence 573, App
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C	37	35.2	1.7	1011	10	US-09-815-242-9734	Sequence 9734, Ap
	38	35.2	1.7	2114	10	US-09-967-768A-188	Sequence 188, App
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C	41	35	1.7	850	12	US-10-042-417-49	Sequence 49, Appl
	42	35	1.7	4139	10	US-09-964-824A-105	Sequence 105, App
	43	35	1.7	4139	10	US-09-964-824A-578	Sequence 578, App
	44	35	1.7	4139	10	US-09-864-864-334	Sequence 334, App
	45	35	1.7	4139	10	US-09-880-107-2121	Sequence 2121, Ap

ALIGNMENTS

RESULT 1
US-09-824-647-16
; Sequence 16, Application US/09824647
; Publication No. US20020183270A1
; GENERAL INFORMATION:
; APPLICANT: Sertero, Ginetle
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; PRIOR APPLICATION NUMBER: 2001-04-04
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
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; SOFTWARE: PatentIn Ver. 2.0
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; NAME/KEY: CDS
; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
; OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank
; OTHER INFORMATION: M75161.
US-09-824-647-16

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; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
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US-09-813-156-16

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DB 1081 CCACAGCTTGAAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 ACCTGCTGCCAATCAGTGTGGGGAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 ACCTGCTGCCAATCAGTGTGGGGAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TGCTCGGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 TGCTCGGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 CAGCGAGAGAGAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CAGCGAGAGAGAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TCCACCCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TCCACCCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TGCCGAGACAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TGCCGAGACAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 GATGCGCAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 GATGCGCAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 AACGACAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 AACGACAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 GCGCCGCTGCGAGCGCTTGAAGGACACGCTTGAAGACAGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 GCGCCGCTGCGAGCGCTTGAAGGACACGCTTGAAGACAGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 GTACTGAAGACTGTCGACGCTTGAAGGACACGCTTGAAGGACAGCTGCTGCTGCTGCTGCTGCT 1860
DB 1801 GTACTGAAGACTGTCGACGCTTGAAGGACACGCTTGAAGGACAGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 CCTAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 CCTAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 GCGAGTGGGGCTCACTTAAGGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980

Db 1921 GGGAGGTGGGCTCAATCAATCAAGCCCTTCCCTGTCAGAGAGGGGTTGAGGAAAAAGCCC 1980
Oy 1981 ATTACAGCTGCATCCCTCCCGTTTCAGTGAACCTGTGGCCAGAGGCTTTTCCCTA 2040
Db 1981 ATTACAGCTGCATCCCTCCCGTTTCAGTGAACCTGTGGCCAGAGGCTTTTCCCTA 2040
Oy 2041 TCCACAGGGGTTTGTGTGTGGGTGTGCTTTCAATAAAGTTTGTACATTCTT 2095
Db 2041 TCCACAGGGGTTTGTGTGTGGGTGTGCTTTCAATAAAGTTTGTACATTCTT 2095

RESULT 3

US-09-824-807-16
; Sequence 16, Application US/09824807
; Patent No. US20020094966A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824.807
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 08/991.862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863.862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Human GP88 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
; OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank
; OTHER INFORMATION: M75161.
US-09-824-807-16

Query Match 100.0%; Score 2095; DB 10; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGCAGGACACCATGTGACCCCTGTGAGCTGGTGGCCCTTAACAGCAGGGGTGTGGCT 60
Db 1 CGCAGGACACCATGTGACCCCTGTGAGCTGGTGGCCCTTAACAGCAGGGGTGTGGCT 60
Oy 61 GGAAGCGGCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 GGAAGCGGCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Oy 121 GGCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 GGCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Oy 181 CTGGGTGGCCCTGCGAGGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 CTGGGTGGCCCTGCGAGGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Oy 241 GTCTAGGAGACTTCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 GTCTAGGAGACTTCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Oy 301 CACTCTGCTCCAGGGGCTTCACATGACAGTGCAGAGGGGAGATCTGCTTCCAAAGATCA 360
Db 301 CACTCTGCTCCAGGGGCTTCACATGACAGTGCAGAGGGGAGATCTGCTTCCAAAGATCA 360
Oy 361 GGTAAACAATCTCGTGGGTGCATTCAGTGCCTGTATAGTACAGTGCATGCATGCATGCATGC 420
Db 361 GGTAAACAATCTCGTGGGTGCATTCAGTGCCTGTATAGTACAGTGCATGCATGCATGCATGC 420
Oy 421 TCCACGCTGTGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

Db 421 TCCACGCTGTGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Oy 481 TGGTGAAGAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 TGGTGAAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Oy 541 CGCTGCATCACACCCAGGGGCAACCCCTGGCAAGAGTCCCTGCCAGAGAGACT 600
Db 541 CGCTGCATCACACCCAGGGGCAACCCCTGGCAAGAGTCCCTGCCAGAGAGACT 600
Oy 601 AACAGGGCAGTGGCTTGTTCACAGCTGGTCAATGTGTCCGAGCAGCAGGTCCGGTCCCT 660
Db 601 AACAGGGCAGTGGCTTGTTCACAGCTGGTCAATGTGTCCGAGCAGCAGGTCCGGTCCCT 660
Oy 661 GATGGTTCACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 GATGGTTCACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Oy 721 GGCACCTGCTGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 GGCACCTGCTGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Oy 781 CAGAGTAACTGCTTCCAGAGGAACCTTACCAGGACCTCTCACTAAGCTGCTGCG 840
Db 781 CAGAGTAACTGCTTCCAGAGGAACCTTACCAGGACCTCTCACTAAGCTGCTGCG 840
Oy 841 CACACAGTGGGAGATGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 CACACAGTGGGAGATGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Oy 901 TGCCTGTACAGTGGGAGGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 TGCCTGTACAGTGGGAGGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 GACCAATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 GACCAATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Oy 1021 CAGGGGCCACACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 CAGGGGCCACACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Oy 1081 CCACAAGCTTGAAGAGATGCTCCCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 CCACAAGCTTGAAGAGATGCTCCCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Oy 1141 ACCTGTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1141 ACCTGTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Oy 1201 TGCCTGAGACACAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 TGCCTGAGACACAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Oy 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Oy 1321 TCCCAACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 TCCCAACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Oy 1381 TGCAGGAGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1440
Db 1381 TGCAGGAGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1440
Oy 1441 GATGCGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 GATGCGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Oy 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

Db	1501	AAGAAATGGTCTCTGACCAAGCTTGGCCACCTTCTG6CCCGGATGACCCCTCAGTGGGTG	1560
Qy	1561	AAGGACCTGGAGTGTGGGGGGAAGAGCACTTCTGGCATGATTAACAGACCTGTGCGGAGAC	1620
Db	1561	AAGGACCTGGAGTGTGGGGGGAAGAGCACTTCTGGCATGATTAACAGACCGTGTGCGGAGAC	1620
Qy	1621	AACCGACAGGGCTGGGCTCTCTCTCTCCCTACAGCCCAAGGCGTGTGTTGTGTAGTGGCGC	1680
Db	1621	AACCGACAGGGCTGGGCTCTCTCTCTCTCCCTACAGCCCAAGGCGTGTGTTGTGTAGTGGCGC	1680
Qy	1681	CACGTGCTCTCTGTGGCTTTCGCTGCGCTGCGAGCGAGGGGTACCAAGTGTTCGGCAGGAG	1740
Db	1681	CACGTGCTCTCTGTGGCTTTCGCTGCGCTGCGAGCGAGGGGTACCAAGTGTTCGGCAGGAG	1740
Qy	1741	GCCTCGGCTGGGAGCGCCCTTGTGAGGGAGCCAGCCTTGACACACTGCTGTGAGGAGCA	1800
Db	1741	GCCTCGGCTGGGAGCGCCCTTGTGAGGGAGCCAGCCTTGACACACTGCTGTGAGGAGCA	1800
Qy	1801	GTACTGAAGACTGTGCAGCCCTCGGGACCCCACTCGSAGGGGTGCCCTGTGCTCAGGCTC	1860
Db	1801	GTACTGAAGACTGTGCAGCCCTCGGGACCCCACTCGSAGGGGTGCCCTGTGCTCAGGCTC	1860
Qy	1861	CCGTGACGCTCCCCCTTAACCAATTCCTCCGTGAGACCCCATCTGTAGCTGCCCATCACAT	1920
Db	1861	CCGTGACGCTCCCCCTTAACCAATTCCTCCGTGAGACCCCATCTGTAGCTGCCCATCACAT	1920
Qy	1921	GGGAGTGGGGGCTCATCTAAAGGCCCTTCCCTGTCAGAAAGGGGTTAGGCAAAAGCC	1980
Db	1921	GGGAGTGGGGGCTCATCTAAAGGCCCTTCCCTGTCAGAAAGGGGTTAGGCAAAAGCC	1980
Qy	1981	ATTTCAAAGCTGCCATCCCTCCCTGTTTCAGTGAGACCTGTGGCAAGGTCTTTCCTTA	2040
Db	1981	ATTTCAAAGCTGCCATCCCTCCCTGTTTCAGTGAGACCTGTGGCAAGGTCTTTCCTTA	2040
Qy	2041	TTCCACAGGGGGTGTGTGTGGTGGGTGCTCTTTCATTAAGTTTGACCTTCTT	2095
Db	2041	TTCCACAGGGGGTGTGTGTGGTGGGTGCTCTTTCATTAAGTTTGACCTTCTT	2095
RESULT 4			
US-09-925-301-574			
Sequence 574, Application US/09925301			
Patent No. US20020052308A1			
GENERAL INFORMATION:			
APPLICANT: Rosen et al.			
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			
FILE REFERENCE: PA106			
CURRENT APPLICATION NUMBER: US/09/925,301			
CURRENT FILING DATE: 2001-08-10			
PRIOR APPLICATION NUMBER: PCT/US00/05882			
PRIOR FILING DATE: 2000-03-08			
PRIOR APPLICATION NUMBER: 60/124,270			
PRIOR FILING DATE: 1999-03-12			
NUMBER OF SEQ ID NOS: 1694			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 574			
LENGTH: 2432			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc.feature			
LOCATION: (7)			
OTHER INFORMATION: n equals a,t,g, or c			
NAME/KEY: misc.feature			
LOCATION: (2326)			
OTHER INFORMATION: n equals a,t,g, or c			
NAME/KEY: misc.feature			
LOCATION: (2367)			
OTHER INFORMATION: n equals a,t,g, or c			
US-09-925-301-574			
Query Match			
96.1%; Score 2014; DB 10; Length 2432;			
Best Local Similarity 99.2%; Pzed. No. 0;			

	Matches 2045; Conservative	0; Mismatches	15; Indels	2; Gaps	2;
QY	1	CGCAGGCGAGCATTGTGACACCTTGCTGAGCTGGTGGCCCTTAAACGACAGGGCTGTGGCT	60		
Db	176	CGCAGGCGAGCATTGTGACACCTTGCTGAGCTGGTGGCCCTTAAACGACAGGGCTGTGGCT	235		
QY	61	GGACGCGGTGCCAAGATGATCAATTTGCTGCTGTGGCCTGTGCTGGACCCGGAGGA	120		
Db	236	GGACGCGGTGCCAAGATGATCAATTTGCTGCTGTGGCCTGTGCTGGACCCGGAGGA	295		
QY	121	GGCAGCTACAGTGGTGGCCGTCCCTTCTTGGAAGAAATGGCCCAACAACATGACAGCAT	180		
Db	236	GGCAGCTACAGTGGTGGCCGTCCCTTCTTGGAAGAAATGGCCCAACAACATGACAGCAT	355		
QY	181	CTGGGTGGGCCCTGGCAGATTGATGCCACACTGCTGTGGCGGCACATCTCGATCTTTAC	240		
Db	356	CTGGGTGGGCCCTGGCAGATTGATGCCACACTGCTGTGGCGGCACATCTCGATCTTTAC	415		
QY	241	GTCTCAGGAGACTTCCAGTTGCTGCCCTTCCAGAAGCCGTGGCATGGCGGGATGGCCAT	300		
Db	416	GTCTCAGGAGACTTCCAGTTGCTGCCCTTCCAGAAGCCGTGGCATGGCGGGATGGCCAT	475		
QY	301	CACCTCTGCCACGGGGCTTCCACTGCAAGTGCAGACGGGCATCTCTTCCAAAGATCA	360		
Db	476	CACCTCTGCCACGGGGCTTCCACTGCAAGTGCAGACGGGCATCTCTTCCAAAGATCA	535		
QY	361	GGTAACAACCTCCGTGGGAGCCATCCAGAGCCCTGATAGTCAGTTGGATGGCCGACATTC	420		
Db	536	GGTAACAACCTCCGTGGGAGCCATCCAGAGCCCTGATAGTCAGTTGGATGGCCGACATTC	595		
QY	421	TTCACGTGCTGTATTAGTGCAGTGGCTCTGGGGGTGCTGGCCCATGCCAGGCTTTC	480		
Db	596	TTCACGTGCTGTATTAGTGCAGTGGCTCTGGGGGTGCTGGCCCATGCCAGGCTTTC	655		
QY	481	TGCTCTGGAAGACAGGGTGCACACTGCTGTCCGACGGTCTTCTGGACCTGGTTACACC	540		
Db	656	TGCTCTGGAAGACAGGGTGCACACTGCTGTCCGACGGTCTTCTGGACCTGGTTACACC	715		
QY	541	CGCTCATACACCCACGGGACACCCACCCCTGGGAAAGAAAGCTCCCTGGCCAGAGACT	600		
Db	716	CGCTCATACACCCACGGGACACCCACCCCTGGGAAAGAAAGCTCCCTGGCCAGAGACT	775		
QY	601	AACAGGGCAGTGGCTTGTCCAGCTCGGATCATGTGTCCGGAGCAGCGGTCCCGGTGCT	660		
Db	776	AACAGGGCAGTGGCTTGTCCAGCTCGGATCATGTGTCCGGAGCAGCGGTCCCGGTGCT	835		
QY	661	GATGGTTTACTGCTGTGAGAGCTGCCCAAGTGGGAATATGGCTGCTGCCAATGCCAAC	720		
Db	836	GATGGTTTACTGCTGTGAGAGCTGCCCAAGTGGGAATATGGCTGCTGCCAATGCCAAC	895		
QY	721	GGCAGCTGTGCTCGATATCACTGCAGTGCACGCCCCCAAGACATGTTGTGACCTGATTC	780		
Db	896	GGCAGCTGTGCTCGATATCACTGCAGTGCACGCCCCCAAGACATGTTGTGACCTGATTC	955		
QY	781	CAGAGTAAGTGCCTTCCAAAGAGAACGCTTACACGAGACTCTTACTTAAGCTGGCTACG	840		
Db	956	CAGAGTAAGTGCCTTCCAAAGAGAACGCTTACACGAGACTCTTACTTAAGCTGGCTACG	1015		
QY	841	CACACAGTGGCGATGTGAATGTGACATGAGAGTGCAGCTGCCAGATGGCTATACCTGC	900		
Db	1016	CACACAGTGGCGATGTGAATGTGACATGAGAGTGCAGCTGCCAGATGGCTATACCTGC	1075		
QY	901	TGCGGTACATAGTGGGGGCGTGGGGCGTGGCCCTTTTACCCAGGCTGTGGCTGTAG	960		
Db	1076	TGCGGTACATAGTGGGGGCGTGGGGCGTGGCCCTTTTACCCAGGCTGTGGCTGTAG	1135		
QY	961	GACCAATACATGTGTGCCCGGGGTTTACGTGTACACGACAAAGGATACCTGTGAA	1020		
Db	1136	GACCAATACATGTGTGCCCGGGGTTTACGTGTACACGACAAAGGATACCTGTGAA	1195		
QY	1021	CAGGGGCCCCACAGTGGCTTGATGTGAGAAAGGCCACGTTACACTTCAGCTTGCAGAC	1080		
Db	1196	CAGGGGCCCCACAGTGGCTTGATGTGAGAAAGGCCACGTTACACTTCAGCTTGCAGAC	1255		

FEATURE:
NAME/KEY: CDS
LOCATION: (23) (1789)
OTHER INFORMATION: The sequence is identical to that of the published
OTHER INFORMATION: mouse granulin except for one nucleotide (T
OTHER INFORMATION: instead of G) at position 1071 of GP88 cDNA
OTHER INFORMATION: (position 1056 of mouse granulin).
US-09-824-807-1

Query Match 57.3%; Score 1200; DB 10; Length 2137;
Best Local Similarity 75.6%; Pred. No. 8e-315;
Matches 1572; Conservative 0; Mismatches 485; Indels 21; Gaps 6;

QY 1 CGCAGCAGACATGAGACCTGAGAGCTGGGCTTAAACAGAGGCTGTGGCT 60
DB 11 CGCAGCAGACATGAGAGCTGTGAGAGCTGGGCTTAAACAGAGGCTGTGGCT 70
QY 61 GGAACGCGGTGCCAGATGCTAGTCTGCTGGCTGTGCTGAGACCCGGAGGA 120
DB 71 GGAACGAGGTCCAGATGAGGAGTCTGCTGGCTGTGCTGAGACCCGGAGGA 130
QY 121 GCCAGGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 131 GCCAGGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
QY 181 CTGGGTGCGCCCTGCCAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 191 CTGAGATGGCTGCTGCCAGACCCAGTGGCTGCTGCTGCTGCTGCTGCTGCT 250
QY 241 GTCTCAGGACTTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 251 GTCTCAGGACTTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 301 CACTGTCGCCAGGCGGCTTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 360
DB 311 CACTGTCGCCAGGCGGCTTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 370
QY 361 GGTACAACTCCGTGGGTGCTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 420
DB 371 G---ATAACCCCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
QY 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 428 GGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
QY 481 TGCCTGAGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 488 TGCCTGAGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
QY 541 CGCTGATACACACCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 548 CGATGCTTACACCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
QY 601 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 608 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 661 GATGTTTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 668 GATGTTTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 721 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 728 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
QY 781 CAGAGTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 788 CAGAGTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
QY 841 CACACAGTGGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 845 TACCCAGTGAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 904

QY 901 TCCGCTCTACAGTGGGCGCTGGGCTGCTGCTGCTTAAACAGAGCTGTGCTGAG 960
DB 905 TCCGCTCTAAACAGTGGGCGCTGGGCTGCTGCTGCTTAAACAGAGCTGTGCTGAG 964
QY 961 GACCAATTAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 965 GATCAATTAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
QY 1021 CAGGCGCCCAACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1025 ATGGGTATCTTCAAGAGTGGTGTATGAAGAGTGTATGAGGCTGCTGCTGCTGCT 1084
QY 1081 CCACAACTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1085 CCACAACTTGAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 1144
QY 1141 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1145 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
QY 1201 TGCCTGAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1205 TGCCTGAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
QY 1261 CAGGAGAGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1265 CAGAGAGAGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
QY 1321 TCCCAACCCAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1325 CTCCAATTTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
QY 1381 TGCCTGAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1385 TGCCTGAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1441 GATGCGAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1445 GATGCGAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
QY 1501 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1505 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 --GATGCTGAGTGTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1618
QY 1621 AACGACAGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1619 AGTGCAGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1678
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1679 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1738
QY 1741 GCCCGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1739 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1798
QY 1801 GTACTGAA-----GACTGTGACGCTGCGGAGCCCACTGCGAGGAGTGCCTGCTC 1853
DB 1799 GCTACAGAGTAAAGAGTCAACAGTCTGCGAGGAGTCAACAGTCTGCTGCTC 1858
QY 1854 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1912
DB 1859 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1918
QY 1913 ATCAATGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1971
DB 1919 ATCAATGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1978
QY 1972 CAAAAGCCATTACAGTGCATGCCCTGCCCTTCAAGTGAACCTGTGGCCAGGTGC 2031

US-09-960-352-6772

Query Match 12.9%; Score 270.4; DB 10; Length 400;
Best Local Similarity 81.8%; Pred. No. 1,1e-63;
Matches 324; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

OY 1 CGCAGGACACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 60
DB 4 CGCAGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 63
OY 61 GGAACCGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 120
DB 64 GGAACCGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 123
OY 121 GGCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 124 GGCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
OY 181 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 184 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
OY 241 GGTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 244 GGTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
OY 301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
DB 304 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
OY 360 AGTAAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 395
DB 364 AGTAAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399

RESULT 11

US-09-960-352-9598
; Sequence 9598, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengling
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9598
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 41-LIB34-036-Q1-E1-C2
US-09-960-352-9598

Query Match 11.3%; Score 236.4; DB 10; Length 398;
Best Local Similarity 79.7%; Pred. No. 1,8e-54;
Matches 279; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 1 CGCAGGACACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 60
DB 49 CGCAGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 108
OY 61 GGAACCGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 120
DB 109 GGAACCGGTGACCATGTGACCTGTGTGAGCTGGGTGACCTTAAACAGCAGGGGTGTGCT 168
OY 121 GGCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 169 GGCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228

OY 181 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 229 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
OY 241 GGTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 289 GGTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
OY 301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
DB 349 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 398

RESULT 12

US-09-864-761-27557/c
; Sequence 27557, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemulca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27557
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003043.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
; OTHER INFORMATION: SWISSPROT HIT: P28799, EVALU6 7.00e-47

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 13:05:13 ; Search time 98 Seconds
(without alignments)
6555.998 Million cell updates/sec

Title: US-08-991-862-16

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1756.6	83.8	1779	2	US-08-429-998-3
4	1756.6	83.8	1779	2	US-08-431-333-3
5	1756.6	83.8	1779	5	PCR-US91-02321-3
6	1200	57.3	2137	4	US-08-991-862-1
7	1142.6	54.5	1767	1	US-07-668-648-1
8	1142.6	54.5	1767	2	US-08-429-998-1
9	1142.6	54.5	1767	2	US-08-431-333-1
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17	396.8	18.9	539	2	US-08-429-998-7
18	396.8	18.9	539	2	US-08-431-333-7
19	396.8	18.9	539	5	PCR-US91-02321-7
20	381.2	18.2	561	4	US-09-404-879A-90
21	139	6.6	561	4	US-09-404-879A-90
22	72.6	3.5	341	1	US-07-668-648-9
23	72.6	3.5	341	2	US-08-429-998-9
24	72.6	3.5	341	2	US-08-431-333-9
25	72.6	3.5	341	5	PCR-US91-02321-9
26	39.2	1.9	1926	4	US-09-249-585A-2
27	39.2	1.9	2580	3	US-09-050-863-2

C	28	39.2	1.9	2580	4	US-09-359-081-2	Sequence 2, Appl
C	29	39.2	1.9	5452	2	US-09-130-114-1	Sequence 1, Appl
C	30	39.2	1.9	9600	4	US-08-910-647-1	Sequence 1, Appl
C	31	39.2	1.9	9600	4	US-09-620-925-1	Sequence 1, Appl
C	32	39.2	1.9	10596	1	US-07-884-811-15	Sequence 15, Appl
C	33	39.2	1.9	10596	1	US-07-885-971-15	Sequence 15, Appl
C	34	39.2	1.9	10596	1	US-08-087-783A-15	Sequence 15, Appl
C	35	39.2	1.9	10596	1	US-08-194-088B-15	Sequence 15, Appl
C	36	39.2	1.9	10596	2	US-08-194-087-15	Sequence 15, Appl
C	37	39.2	1.9	10596	5	PCR-US93-04648-15	Sequence 15, Appl
C	38	38.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C	39	38	1.8	2742	1	US-08-911-853-16	Sequence 16, Appl
C	40	38	1.8	2742	4	US-09-479-409-16	Sequence 16, Appl
C	41	38	1.8	17612	3	US-08-911-853-16	Sequence 16, Appl
C	42	38	1.8	17612	4	US-09-479-409-16	Sequence 16, Appl
C	43	38	1.8	17612	4	US-09-479-409-29	Sequence 29, Appl
C	44	38	1.8	17612	4	US-09-479-453-29	Sequence 29, Appl
C	45	37.6	1.8	3183	1	US-08-849-212-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-991-862-16
; Sequence 16, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Human GP88 CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
; OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank
; OTHER INFORMATION: M75161.
US-08-991-862-16

Query Match
Best Similarity 100.0%; Score 2095; DB 4; Length 2095;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCAGCAGACCATGTGACCTGTGAGCTGGGTGACCTTAACAGAGGCTGTGCT	60
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QY	61	GGAACGGGGGCCAGATGTGCACTTGTGCTGGGCTGCTGACCCCGGAGGA	120
DB	61	GGAACGGGGGCCAGATGTGCACTTGTGCTGGGCTGCTGACCCCGGAGGA	120
QY	121	GCCAGTACAGCTGTGCTGCTCCCTTCTGGACAAATGCGCCCAACATGACAGCAT	180
DB	121	GCCAGTACAGCTGTGCTGCTCCCTTCTGGACAAATGCGCCCAACATGACAGCAT	180
QY	181	CTGGGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240
DB	181	CTGGGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240
QY	241	GTCACAGGAGCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	300
DB	241	GTCACAGGAGCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	300

OY	301	CACGCTGCCCCACGGGGCTTCACATGCAATGAGACAGGGGGATCCGCTTCCAAAGATCA	360
Db	301	CACGCTGCCCCACGGGGCTTCACATGCAATGAGACAGGGGGATCCGCTTCCAAAGATCA	360
OY	361	GGTAAACAATCCGTTGGGTGCCATTCACATGCCCCGTATAGTCAGTTGGAAATGCCGGAGATTC	420
Db	361	GGTAAACAATCCGTTGGGTGCCATTCACATGCCCCGTATAGTCAGTTGGAAATGCCGGAGATTC	420
OY	421	TCCAAGTGTCTGTATTATGTGTGATATGGCTCTGGGGGGTGGCTGGCCCCATGCCCCAGGCTTCC	480
Db	421	TCCAAGTGTCTGTATTATGTGTGATATGGCTCTGGGGGGTGGCTGGCCCCATGCCCCAGGCTTCC	480
OY	481	TGCTGTGAAGACAGGGGTGCATGCTGTGCCAGAGGGTGGCCCTGCGACACCTGGTTACACAC	540
Db	481	TGCTGTGAAGACAGGGGTGCATGCTGTGCCAGAGGGTGGCCCTGCGACACCTGGTTACACAC	540
OY	541	CGCTGCATCACACCCACAGGGGACCCACCCCCCTGGCAAAGACGCTCCCTCCAGAGAGACT	600
Db	541	CGCTGCATCACACCCACAGGGGACCCACCCCCCTGGCAAAGACGCTCCCTCCAGAGAGACT	600
OY	601	AACAGGCGATGTGGCTTGTCCAGCTGGGTATGTGTCCGAGCGACAGGGTCCGGTGGCCCT	660
Db	601	AACAGGCGATGTGGCTTGTCCAGCTGGGTATGTGTCCGAGCGACAGGGTCCGGTGGCCCT	660
OY	661	GATGGTTCTACCTCTGTGAGCTGGCCAGTGGGGAATATGGGTGGCGGCCCATGCCCCAAC	720
Db	661	GATGGTTCTACCTCTGTGAGCTGGCCAGTGGGGAATATGGGTGGCGGCCCATGCCCCAAC	720
OY	721	GCCACCTGCTCTCCGATTCACCTGTGCATGCTGGCCCCAGACACCTGTGTATACCTGTATC	780
Db	721	GCCACCTGCTCTCCGATTCACCTGTGCATGCTGGCCCCAGACACCTGTGTATACCTGTATC	780
OY	781	CAGAGTAAGTGCTCTCTCCAAAGAGAACGCTACACGGACCTCTCTACTAAGCTGCTGGCG	840
Db	781	CAGAGTAAGTGCTCTCTCCAAAGAGAACGCTACACGGACCTCTCTACTAAGCTGCTGGCG	840
OY	841	CACACAGTGGGGCGATTGGAAATGTGACATGAGAGTGAAGTGGCCAGATGAGATACCTGC	900
Db	841	CACACAGTGGGGCGATTGGAAATGTGACATGAGAGTGAAGTGGCCAGATGAGATACCTGC	900
OY	901	TGCGGTACAGTTCGGGGGGCTGTGGGCTGCTGCCCTTTTACCAGAGCTGTGTGCTGTAG	960
Db	901	TGCGGTACAGTTCGGGGGGCTGTGGGCTGCTGCCCTTTTACCAGAGCTGTGTGCTGTAG	960
OY	961	GACCAATACACTGCTGTCCCCGGGGGTTTACGTGTGACACGACGAGAGGGTACCTGTGAA	1020
Db	961	GACCAATACACTGCTGTCCCCGGGGGTTTACGTGTGACACGAGAGAGGGTACCTGTGAA	1020
OY	1021	CAGGGGCCCCACAGGTGGTCCCTGGATGGAAAGGGCCCCAGCTACCTCAAGCTCTGGCAGAC	1080
Db	1021	CAGGGGCCCCACAGGTGGTCCCTGGATGGAAAGGGCCCCAGCTACCTCAAGCTCTGGCAGAC	1080
OY	1081	CCACAAGCTTTGAAGAGAGATGTTCCTCTGTGATAATGTACAGAGCTGTCCCTCTCCGAT	1140
Db	1081	CCACAAGCTTTGAAGAGAGATGTTCCTCTGTGATAATGTACAGAGCTGTCCCTCTCCGAT	1140
OY	1141	ACCTGTCTCCCACTTCACGCTGTGGGGAGTGGGGCTGTGTCCAAATCCACAGAGGCTGTGCG	1200
Db	1141	ACCTGTCTCCCACTTCACGCTGTGGGGAGTGGGGCTGTGTCCAAATCCACAGAGGCTGTGCG	1200
OY	1201	TGCTGTGGACCCACAGCACTCTCTCCCCCAGCGATTACACATGTGTAGCTGAAGGGGACAGGT	1260
Db	1201	TGCTGTGGACCCACAGCACTCTCTCCCCCAGCGATTACACATGTGTAGCTGAAGGGGACAGGT	1260
OY	1261	CAGGAGAGAAACGAGATCTGTGGCTGTGACCTGTGAAATCATCTGTGCCGGCGGGTTCCTTA	1320
Db	1261	CAGGAGAGAAACGAGATCTGTGGCTGTGACCTGTGAAATCATCTGTGCCGGCGGGTTCCTTA	1320
OY	1321	TCCCAACCCACAGACATCTGGCTGTGACACAGCACACCAAGCTGGCCGGTGGCGGAACCTGC	1380
Db	1321	TCCCAACCCACAGACATCTGGCTGTGACACAGCACACCAAGCTGGCCGGTGGCGGAACCTGC	1380
OY	1381	TGCCGAGACCAAGGTTGGGAGCTGGGCCCTGCTGCCAGTTGCCCAATGCTGTGTGGTCGAG	1440

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Db      1381  TCCCGGACCGAGGGGTGGGAGCTGGGAGCTGCTGCCAATTGCCCCATTCGTGTGTGCTGCAG  1440
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Qy      1441  GATGCGCAGCACTGCTGCCGCGGTGGCTGGCTACACCTGCACAGCTGAAGGCTGATCTGCGAG  1500
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Db      1441  GATGCGCAGCACTGCTGCCGCGGTGGCTGGCTACACTGCACAGCTGAAGGCTGATCTGCGAG  1500
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Qy      1501  AAGAAGTGTGTCTGTGCCCAAGCTTGCCACACTTCTCTTGCCCGTAGGCCCTTCACGTGGGTGTG  1560
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Db      1501  AAGGAAGTGTGTCTGTGCCCAAGCTTGCCACACTTCTCTTGCCCGTAGGCCCTTCACGTGGGTGTG  1560
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Qy      1561  AAGGACGTGGAGTGTGGGGAAGGACAATTGTGCATGATTAACAGACCGTGCCTGCGCGAGAC  1620
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Db      1561  AAGGACGTGGAGTGTGGGGAAGGACAATTGTGCATGATTAACAGACCGTGCCTGCGCGAGAC  1620
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Qy      1621  AACCGACAGGGGCTGGGCGCTGCTGTCCCTAACGCCCAAGGGGCTGTGTTGCTCATGCGCGC  1680
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Db      1621  AACCGACAGGGGCTGGGCGCTGCTGTCCCTAACGCCCAAGGGGCTGTGTTGCTCATGCGCGC  1680
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Qy      1681  CACTGCTCTCTGCTGTGCTTCCTCCGTGCGACGACGAGGGGTACCAAGTGTTCGCGAGGGAG  1740
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Db      1681  CACTGCTCTCTGCTGTGCTTCCTCCGTGCGACGACGAGGGGTACCAAGTGTTCGCGAGGGAG  1740
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Qy      1741  GCCCGCGGCTGGGACGCCCTTTGAGGAGACCAGCTTGAGACAGCTGCTGTGAGGAGACA  1800
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Db      1741  GCCCGCGGCTGGGACGCCCTTTGAGGAGACCAGCTTGAGACAGCTGCTGTGAGGAGACA  1800
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Qy      1801  GTACTGAAGACTGTGCAGACCCCTGGGAGCCCACTGCGAGGGGAGCCCTGTGCTCAGGCGTC  1860
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Db      1801  GTACTGAAGACTGTGCAGACCCCTGGGAGCCCACTGCGAGGGGAGCCCTGTGCTCAGGCGTC  1860
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Db      1861  CCTAGCACTCTCCCCTTAAACCAAATTTCTCCCTGGAGCCCAATTCGTGAGCTCCCATCACAT  1920
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Qy      1921  GGGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAAGGGGGTTAGAGCAAAAGGCC  1980
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Db      1921  GGGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTCAGAAAGGGGGTTAGAGCAAAAGGCC  1980
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Qy      1981  ATTACAACTCCATCCATCCCTTACCCCGTTTCAGTGGAGACCTGTGGCAGAGTGCTTTCCCTA  2040
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Db      1981  ATTACAACTCCATCCATCCCTTACCCCGTTTCAGTGGAGACCTGTGGCAGAGTGCTTTCCCTA  2040
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Qy      2041  TTCACAGGGGTGTGTGTGTGTGTGGGTGTGCTTCAATAAAGTTGTCACTTTCTT  2095
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Db      2041  TTCACAGGGGTGTGTGTGTGTGTGGGTGTGCTTCAATAAAGTTGTCACTTTCTT  2095
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RESULT 2
US-07-668-3
; Sequence 3, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
;   APPLICANT: Shoyab, Mohammed
;   TITLE OF INVENTION: EPIHELINS: NOVEL CYSTEINE-RICH GROWTH
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 19910819

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Db 1321 GACATGGCTGTACACGACACACACCTGCGGGGAGACCTGTGCGGACCTG 1380
Qy 1393 GGTGGAGCTGGGCTGTGCTGACAGTTCATGCTGTGTGCTGCGAGATGCGACAC 1452
Db 1381 GGTGGAGCTGGGCTGTGCTGACAGTTCATGCTGTGTGCTGCGAGATGCGACAC 1440
Qy 1453 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512
Db 1441 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 1513 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1572
Db 1501 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1573 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1632
Db 1561 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Qy 1633 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1692
Db 1621 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1693 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1752
Db 1681 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1753 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
Db 1741 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779

RESULT 4
US-08-431-333-3
Sequence 3, Application US/0841333
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plovman, Gregory D.
TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1779
US-08-431-333-3
Query Match 83.8%; Score 1756.6; DB 2; Length 1779;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 13 ATGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 72
Db 1 ATGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Qy 73 CCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
Db 61 CCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 133 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
Db 121 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 193 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
Db 181 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 253 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
Db 241 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 313 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
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Db 361 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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Db 481 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 553 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Db 541 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 613 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
Db 601 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 673 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 661 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 733 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
Db 721 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 793 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 852
Db 781 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 853 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
Db 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

OY	913	TCGGGGGCTCGGGGCTCGCTCCCTTTTACCGAGGCTGTGTGGTGGAGACCACTATAC	972
Db	901	TCGGGGGCTCGGGGCTCTCTCCCTTTTACCGAGGCTGTGTGGTGGAGACCACTATAC	960
OY	973	TGCTGTCCCGGGGTTTACGTGTGACAGCAGAAAGGTAACCTGTGTAACAGAGGGCCAC	1032
Db	961	TGCTGTCCCGGGGTTTACGTGTGACAGCAGAAAGGTAACCTGTGTAACAGAGGGCCAC	1020
OY	1093	CAGGTGGCTGTGAGTGAAGAGGGCCGACACCTTAGCTGTGCGACACCAAGCTTG	1092
Db	1021	CAGGTGGCTGTGAGTGAAGAGGGCCGACACCTTAGCTGTGCGACACCAAGCTTG	1080
OY	1093	AAGAGAGTGTCCCTCTGTATATGTACAGAGCTGTCCCTCCCGATACCTGTGTCCAA	1152
Db	1081	AAGAGAGTGTCCCTCTGTATATGTACAGAGTGTCCCTCCCGATACCTGTGTCCAA	1140
OY	1153	CTCACGTCTGTGGGAGTGTGGGCTCTGTCCAATCCAGAGAGCTGTCTGCTGGACAC	1212
Db	1141	CTCACGTCTGTGGGAGTGTGGGCTCTGTCCAATCCAGAGAGCTGTCTGCTGGACAC	1200
OY	1213	CAGACTGTGTGCCCCCGACATACAGTGTGTAGTGAAGGGGCACTGTACAGAGGAAGC	1272
Db	1201	CAGACTGTGTGCCCCCGAGGCTACAGTGTGTAGTGAAGGGGCACTGTACAGAGGAAGC	1260
OY	1273	GAGATCGTGTGGCTGTGAGTGAAGAGATGCTGTGCCCGCGGGTTCCTTATCCACCCAGA	1332
Db	1261	GAGATCGTGTGGCTGTGAGTGAAGAGATGCTGTGCCCGCGGGTTCCTTATCCACCCAGA	1320
OY	1333	GACATCGGCTGTGACCAAGCACACACACTTCCCGTGTGGGGGAACCTGTGCCCAAGCCAG	1392
Db	1321	GACATCGGCTGTGACCAAGCACACACACTTCCCGTGTGGGGGACACCTGTGCCCAAGCTG	1380
OY	1393	GGTGGGAGCTGTGGGCTGTCTCCAGTTGGCCCATGTGTGTGTGGAGGATGTGCCAGAC	1452
Db	1381	GGTGGGAGCTGTGGGCTGTCTCCAGTTGGCCCATGTGTGTGTGGAGGATGTGCCAGAC	1440
OY	1453	TGCTGTCCCGGCTGTGCTATACACTTGCACAGTGAAGGCTTCATCTGTGGAGAAAGAGTGTCT	1512
Db	1441	TGCTGTCCCGGCTGTGCTATACACTTGCACAGTGAAGGCTTCATCTGTGGAGAAAGAGTGTCT	1500
OY	1513	TCTGTCCAGGCTGTGCACACTTCTGTGGCCGCTGTAGCCCTTCACAGTGGTGTGAAGAGCTGTGAG	1572
Db	1501	TCTGTCCAGGCTGTGCACACTTCTGTGGCCGCTGTAGCCCTTCACAGTGGTGTGAAGAGCTGTGAG	1560
OY	1573	TGTGTGGGAGAGACACTTCTGTCCATGTATTAACAGACCTGTCTGCTGCCAGACACCGACAGGC	1632
Db	1561	TGTGTGGGAGAGACACTTCTGTCCATGTATTAACAGACCTGTCTGCTGCCAGACACCGACAGGC	1620
OY	1633	TGGGCTGTGTGTCCCATACGCGCCAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1692
Db	1621	TGGGCTGTGTGTCCCATACGCGCCAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1680
OY	1693	GCTGT	1752
Db	1681	GCTGT	1740
OY	1753	GAGCGCCCTTTGAGAGGACCAAGCTTTGAACAGACTGTCTG	1791
Db	1741	GAGCGCCCTTTGAGAGGACCAAGCTTTGAACAGACTGTCTG	1779

RESULT 5
PCT-US91-02321-3
; Sequence 3, Application PC/TUS9102321

1 APPLICANT: Shoyab, Mohammed
2 APPLICANT: Plozman, Gregory D.
3 TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
4 TITLE OF INVENTION: MODULATING PROTEINS
5 NUMBER OF SEQUENCES: 12
6
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Bristol-Myers Squibb Company

```

1 STREET: 3005 First Avenue
2 CITY: Seattle
3 STATE: Washington
4 COUNTRY: USA
5 ZIP: 98121
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: PCT/US91/02321
14 FILING DATE: 19910403
15 CLASSIFICATION: 514
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Poor, Brian W.
18 REGISTRATION NUMBER: 32,928
19 REFERENCE/DOCKET NUMBER: ON071A-PC
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (206)728-4800
22 TELEFAX: (206)448-4775
23 INFORMATION FOR SEQ ID NO: 3:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 1779 base pairs
26 TYPE: NUCLEIC ACID
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 MOLECULE TYPE: cdna
30 ORIGINAL SOURCE:
31 ORGANISM: Homo sapiens
32 TISSUE TYPE: Kidney
33 FEATURE:
34 NAME/KEY: CDS
35 LOCATION: 1..1779
36 PCT-US91-02321-3

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Query Match	83.88;	Score 1756.6;	DB 5;	Length 1779;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 1765;	Conservative	0;	Mismatches 14;	Indels 0;
			Gaps	0;

QY	13	ATGTGGACCCGTGGAGCTGGGTGGACCTTAACACACAGGGCTGGGTGGAAACGGGTGC	72
Dp	1	ATGTGGACCCGTGGAGCTGGGTGGACCTTAACACACAGGGCTGGGTGGAAACGGGTGC	60
QY	73	CCAGATGCTCAGTTCGTGCGCTGTGGCTGTGGCTGGACCCCGGAGAGCCACGTACAGC	132
Dp	61	CCAGATGCTCAGTTCGTGCGCTGTGGCTGTGGCTGGACCCCGGAGAGCCACGTACAGC	120
QY	133	TGCTGCCCTCCCTTCCTTGAGCAATATGGGCCCAACACACTGGACAGGCACTCTGGGTGGCCCC	192
Dp	121	TGCTGCCCTCCCTTCCTTGAGCAATATGGGCCCAACACACTGGACAGGCACTCTGGGTGGCCCC	180
QY	193	TGCCAGGTTGATGGCCCACTGCTCTGGCGGCACACTCTGACATCTTTTACCGTCTCAGGAGCT	252
Dp	181	TGCCAGGTTGATGGCCCACTGCTCTGGCGGCACACTCTGACATCTTTTACCGTCTCAGGAGCT	240
QY	253	TCCAGTTGCTGCCCCCTTCCAGAGAGCCGTGGCCAGCGGGGATGGCCATCACTGCTGCCA	312
Dp	241	TCCAGTTGCTGCCCCCTTCCAGAGAGCCGTGGCCAGCGGGGATGGCCATCACTGCTGCCA	300
QY	313	CGGGGCTTCCACTGCAGTGCAGAGCGGGCGATCTGCTTCCAAAGATCAGGTAAACAATCC	372
Dp	301	CGGGGCTTCCACTGCAGTGCAGAGCGGGCGATCTGCTTCCAAAGATCAGGTAAACAATCC	360
QY	373	GTGGGTGCCATCCAGTGCCTCGATATGATCAGTTGCAATGCCCCGAGCTTCTCCAGTGTCTG	432
Dp	361	GTGGGTGCCATCCAGTGCCTCGATATGATCAGTTGCAATGCCCCGAGCTTCTCCAGTGTCTG	420
QY	433	GTTATTTGGCATTTGGCTCTCTGGAGGTGGTGGCCCCATGGCCCCAGAGTTCTCTGTGGAAAG	492
Dp	421	GTTATTTGGCATTTGGCTCTCTGGAGGTGGTGGCCCCATGGCCCCAGAGCTTCTCTGTGGAAAG	480
QY	493	AGGGTGCACCTGTGCGGACAGGTGACCTTCTGCGACCTGGTTACACACCCCGCTCATACA	552

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Db 481 AGGATGACATGCTGTCGACAGGTGCTTCTGAGACTGGTTACACCCGCTCATCAC 540
Oy 553 CCCAGGGGACCCACCCCTGGCAAGAGAGTCCCTGCCAGAGAGCTAAACAGGGCAGT 612
Db 541 CCCAGGGGACCCACCCCTGGCAAGAGAGTCCCTGCCAGAGAGCTAAACAGGGCAGT 600
Oy 613 GCGTGTCCAGTGGTGCATGTGTCCGAGGACAGGATCCCGGTGCCCTGATGGTTTACC 672
Db 601 GCGTGTCCAGTGGTGCATGTGTCCGAGGACAGGATCCCGGTGCCCTGATGGTTTACC 660
Oy 673 TGGTGTGAGACTGCCAGTGGGAGATGTGGTGTGCCAATGGCCAAAGCCACTGTGTC 732
Db 661 TGGTGTGAGACTGCCAGTGGGAGATGTGGTGTGCCAATGGCCAAAGCCACTGTGTC 720
Oy 733 TCCGATCACCCTGACATGTGCCCCCAAGACACTGTGTGAGCTGTATCCAGATTAAGTGC 792
Db 721 TCCGATCACCCTGACATGTGCCCCCAAGACACTGTGTGAGCTGTATCCAGATTAAGTGC 780
Oy 793 CTCTCCAGAGAGAACGCTACACAGGACCTCTCCTCACTAAGCTGCCCTGCGCACAGTGGGC 852
Db 781 CTCTCCAGAGAGAACGCTACACAGGACCTCTCCTCACTAAGCTGCCCTGCGCACAGTGGGC 840
Oy 853 GATGTAAATGTGACATGAGAGTGGAGTGGCTGCGCATATACCTGCTGCTCTACAG 912
Db 841 GATGTAAATGTGACATGAGAGTGGAGTGGCTGCGCATATACCTGCTGCTCTACAG 900
Oy 913 TCGGGGGCCCTGGGGCTGTGCCCCCTTTTACCAGAGCTGTGTGGCTGTGAGGACCATATAC 972
Db 901 TCGGGGGCCCTGGGGCTGTGCCCCCTTTTACCAGAGCTGTGTGGCTGTGAGGACCATATAC 960
Oy 973 TGGTGTCCCGGGGGTTTACGTGTGACAGGACGACAGAGGATACCTGTATACAGGGGCCAC 1032
Db 961 TGGTGTCCCGGGGGTTTACGTGTGACAGGACGACAGAGGATACCTGTATACAGGGGCCAC 1020
Oy 1033 CAGGTCCCTGGATGAGAGAGGCCCAAGCTCACCCTGACCTGCGACAGCCACAGCTTG 1092
Db 1021 CAGGTCCCTGGATGAGAGAGGCCCAAGCTCACCCTGACCTGCGACAGCCACAGCTTG 1080
Oy 1093 AAGAGAGATGTCCCTGTGTATGTACAGAGCTGTCCCTCCGCGATATACCTGTGCCAA 1152
Db 1081 AAGAGAGATGTCCCTGTGTATGTACAGAGCTGTCCCTCCGCGATATACCTGTGCCAA 1140
Oy 1153 CTACAGCTGTGGGAGTGGGGCTGCTGTCCAAATCCAGAGGCTGTGCTGTGCGACAC 1212
Db 1141 CTACAGCTGTGGGAGTGGGGCTGCTGTCCAAATCCAGAGGCTGTGCTGTGCGACAC 1200
Oy 1213 CAGCACTGTGCCCCCAAGGATACAGCTGTGTGTGTGAGGGGCAGTGTACGCGAGAGC 1272
Db 1201 CAGCACTGTGCCCCCAAGGATACAGCTGTGTGTGTGAGGGGCAGTGTACGCGAGAGC 1260
Oy 1273 GAGATGTGGGCTGTGAGAGATGAGCTGCCCCGCGCGGCTTCATATCCACCCACA 1332
Db 1261 GAGATGTGGGCTGTGAGAGATGAGCTGCCCCGCGCGGCTTCATATCCACCCACA 1320
Oy 1333 GACATGGGTGTGACAGACACACAGCTGCCGCGGTGGGCGAACTGTGTCGCCAGAC 1392
Db 1321 GACATGGGTGTGACAGACACACAGCTGCCGCGGTGGGCGAACTGTGTCGCCAGAC 1380
Oy 1393 GGTGGGAGCTGGGGCTGTGCTGCCAGTGTGCCCATGTGTGTGTGCGAGAGATGGCCAGAC 1452
Db 1381 GGTGGGAGCTGGGGCTGTGCTGCCAGTGTGCCCATGTGTGTGTGCGAGAGATGGCCAGAC 1440
Oy 1453 TGGTGTCCCGGCTGTACACCTGCAAGTGAAGGCTGATCCTGCGAGAGAGAGTGGTC 1512
Db 1441 TGGTGTCCCGGCTGTACACCTGCAAGTGAAGGCTGATCCTGCGAGAGAGAGTGGTC 1500
Oy 1513 TGTGCCAGGCTGCAACTTCTGCGCCGCTGAGCCCTCACGTGGGTGTGAAGGAGCTGGAG 1572
Db 1501 TGTGCCAGGCTGCAACTTCTGCGCCGCTGAGCCCTCACGTGGGTGTGAAGGAGCTGGAG 1560
Oy 1573 TGTGGGAGAGGACATTTCTGCGCATATACCAACTGCTGCGGAGACAAACGAGAGGC 1632

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Db 1561 TGTGGGAGAGGACATTTCTGCCATGATMACAGACTGCTGCCGAGACAAACGAGAGGC 1620
Oy 1633 TGGGCTGTGTCCTTACAGCCAGGCGCTGTGTGTGTGATGAGGCGCACTGTGCT 1692
Db 1621 TGGGCTGTGTCCTTACAGCCAGGCGCTGTGTGTGTGATGAGGCGCACTGTGCT 1680
Oy 1693 GCTGCTTCCGCTGCGACAGGAGGTACCAAGTGTGTGTGCGAGGAGGCCCGCTGG 1752
Db 1681 GCTGCTTCCGCTGCGACAGGAGGTACCAAGTGTGTGTGCGAGGAGGCCCGCTGG 1740
Oy 1753 GAGGCCCCCTTGAAGGAGCCAGGCTGTGAGACACTGCTG 1791
Db 1741 GAGGCCCCCTTGAAGGAGCCAGGCTGTGAGACACTGCTG 1779

RESULT 6
US-08-991-862-1
; Sequence 1, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996 488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Mouse epithelin/granulin
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(1789)
; OTHER INFORMATION: The sequence is identical to that of the published
; OTHER INFORMATION: mouse granuln except for one nucleotide (T
; OTHER INFORMATION: instead of G) at position 1071 of gp88 cDNA
; OTHER INFORMATION: (position 1056 of mouse granuln).
US-08-991-862-1

Query Match          57.3%; Score 1200; DB 4; Length 2137;
Best Local Similarity 75.6%; Pred. No. 8e-292;
Matches 1572; Conserved 0; Mismatches 485; Indels 21; Gaps 6;

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OY	421	TCGACGCGTGTGTTATGTCACATGGCTCTGGGGGTGCTGGCCATGCCACAGGCTTCC	480
OY	428	GGCACTGCTGCATTTATGTTGTAATGGTGTGCGGGATGTTGTTCCATGCTGCCAGGCTCT	487
OY	481	TGCTGTGAAAGCAGGGTGCATCTGCTGCGCACAGGTGCTTCTGCGACCTGGTTACACC	540
OY	488	TGCTGTGAAAGCAGAGTGCATTTGCTGTCCCAATGGGGGCTCTCTGTAGCTGGTTACACA	547
OY	541	CGCTGCATACACCCACAGGGGACCACCCCTGGCGAATAAAGCTCCCTGCCACAGAGACT	600
OY	548	CGATGCGTTTACCCACAGGGGACCACACCCCTACTAAAGATTTCCCTGCACAAAAGACC	607
OY	601	AACAGGGCAGTGGGCTTGTCCAGCTGATGTGCCGAGCAGCAGGTCGGGTGCTT	660
OY	608	AACAGCGCAGTGTGTTTGGCTTTTTCGTGTGTGTGCTCGCATGATGTAAGACCGAGTGTCC	667
OY	661	GATGCTTCTACCTCTGTGTAGCTGCCAGTGGGAATATGCTGCTGCCCAATGCCCAAC	720
OY	668	GATCATTTCTACCTCTGTGTAGCTACCCACATGGGAAATATGGTGTGTCCATGTCCCAAT	727
OY	721	GGCACTGCTCTCCGATTCACCTGCATGTGCTGCCCAAGACATGTGTGATCCTGTATC	780
OY	728	GGCATCTGTCTTTCGACACACTGCATCTGTGCCCCAGAGACATGTATGTATCCTGTATC	787
OY	781	CAGAGTAAGTCTCTTCCAAAGAGAAACGCTACCAAGGACCTCTCTACTAAGTCTGCTCG	840
OY	788	CAGAGTAAGTCTCTTCCAAAGAGAAACGCTACCAAGGACCTCTCTACTAAGTCTGCTCG	844
OY	841	CACACAGTGGGCGATGTGAAATGTGCATGTGGAGTGTGCTGCCAGATGGGCTATACCTGC	900
OY	845	TACCCATGTGAAGAGGTGGAAGTGCAGCATGTAGAGTATGCTGCCCTGTGAAGATATACCTGC	904
OY	901	TGCGGTCTACAGTGGGGGCTGCGGCTGTGCTCCCTTTTACCAGGCTGTGTGTGTAG	960
OY	905	TGCGGCTCAACACTGTGGGGCTGTGGGCTGTGTCTTCATTGTCCAAAGCGTGTGTGTAG	964
OY	961	GACCACTATACACTGCTGTCCCGGGGGTTTACGTGTGAACCCAGCAAGGATACCTGTGAA	1020
OY	965	GATCATCTCTCTCTCCCGGCAAGGTTTCACTGTGCACACAGAGAAAGAACTGTGCAAA	1024
OY	1021	CAGGGGCCCCACAGGTGCCCTGGATGTGAAAGGCCCCACAGCTACCTCAGCTGTGCACAC	1080
OY	1025	ATGGGTATCCTCAAGTAAAGGTGGAATGAAAGAAAGTCATAGCCCCCTCGCTGTGCACAC	1084
OY	1081	CCACAAAGCTTTGAAGAAAGATGTCCCTGTGTGATATGTACAGACGTGTCCCTTCCTGCAT	1140
OY	1085	CCACAGATCTTTGAAGATGTATACCTGTGTGATGACTTACTAAGGTTGCTTCAAAACAAT	1144
OY	1141	ACTGTCTCCAACTCAGCTGTGGGGAGTGGGGCTGTGTCTCAATGCCAAGAGGCTGTGC	1200
OY	1145	ACCTGTCTCAAACTCATTTCTGGGGAGCTGGGGCTGTGTCTCCATGCCAAGAGGCTGTGC	1204
OY	1201	TGCTGGACACACAGCACTGCTGCCCCACAGCATACAGTGTGTAGTGAAGGGGAGTGT	1260
OY	1205	TGCTTAGACAACTCAGCAATTGCTGCCCTCAGAGGCTTACATGTCTGGCTCAGGGGATCTGT	1264
OY	1261	CAGCGAGGAAGCGAGTGTGGGTGTGACATGTGAGAAATATCGTGGCCCCGCGGCTTCTTA	1320
OY	1265	CAGAAAGGAGACACATATGTGGTGTGGCTGTGGAATAATACGTGCCCGCCAGACAAACCCG	1324
OY	1321	TCGCACCCCAAGACATCTGGCTGTGCACAGACACACAGTGTGCCGGTGGCGGAACCTGC	1380
OY	1325	CTCCAAATTTGAGATATTCGGTTGTGAAACAGCAATACCAGTGTGCCAGTATAGGCGAACTGC	1384
OY	1381	TGCCGAGCCACAGGGTGGAGCTGGGCTGTGTGCATGTGCCCATGTCTGTGTGTGCGAG	1440
OY	1385	TGCCCAAGCCTCAAGGGGAATGTGGGCTGTGTGCACACTCCCAATGTCTGTGTGTGAG	1444
OY	1441	GATGGCCAGCACTGTGCTCCGGGTGGCTACACTGTGAACGTAAAGCTGATCCCTGGAG	1500
OY	1445	GACCGGACGACTTGTGCCGGGCGGGTACACTGTCAAGCTAAAGTAAAGCCGAGACCTGTGAG	1504

Oy	1501	AAGGAAAGGACCTCTGGCCAGACCGTCCACTTCCTCTGGCCGTAAGGCCTACGTGGGTGTG	1560
Db	1505	AAGGATGTCCATTTTATCCAGACCTCCCGTGTCTCTACCTCTGGCCCTAAGSTGTG----	1560
Oy	1561	AAGGACGTGAGTGTGGGGAAAGGACAACTTCGTGCATGATATACCAGACCTGCTGCCGAGAC	1620
Db	1561	--GAATGTGGAGTGTGGAGAAAGGACATTTCTGCGCATGATATACAGACCTGTTGTAAACAC	1618
Oy	1621	AACCGACAGGGCTGGCCCTGCTGCTCCCTACGCCAGGGCGTGTGTGTGCTATCGCGC	1680
Db	1619	AGTCAGAGAGTGTGGGCTGCTGCTGCTCCCTACCTAAAGGGTGTGCTGTAGAGATGACGT	1678
Oy	1681	CACGTGTCCTGTGCTGGCTTCGCGTGGGACGAGGGGTACCAAGTGTGGCGAGGGAG	1740
Db	1679	CACGTGTGCCCCGGTGGCTTCCACTGTTCACCGAGGGGAAACAAAGTGTGGAAAGAG	1738
Oy	1741	GCCTCCGGCTGGAGCGCCCTTTGAGGGACCCAGCCTTACAGACGTGCTGTAGAGGACA	1800
Db	1739	ATTCTCTGGCTGGGACATGTTTGTGAGGATCCGGTGTCCAAAGACGCTACTGTATAGGAAG	1798
Oy	1801	GTACTGAA-----GACTGTGACGCCCTTCGGGACCCCACTCGAGGGTCCCTCTGCTC	1853
Db	1799	GCTACAGACTTAAAGAGACTCCACAGTCTGTGGAAACCTGTCCGAGGGATACCACTACTAC	1858
Oy	1854	AGGCTCTCCCTAGACACTCCCCCTTAACCAATTTCTCCTGAGACCACTTGTAG--CTCCCC	1912
Db	1859	AGGCTCTCCCTAGCCCTCTCTCCCTTAACGTCTCCCGGCTACTACTCTGTAGTATACCT	1918
Oy	1913	ATCACATGGAGGTGGGCGCTCAATCTTAGAGCCCTTCCTCTGACAGAAAGGGGTTGAGG-	1971
Db	1919	ATCACATGGGAGGTGGAGCTCAAACTTAACCTCTTTTATGGAAGAAAGGCTCTGGC	1978
Oy	1972	CAAAAAGCCCATTTACAAAGCTGCCATCCCTCCCGCTTTCATGATGAGACCTGTGGCCAGGTGC	2031
Db	1979	CAAAAAGCCCATTTACAAAGCTGCCATTTCTTCCGGTTTCTGTGAGACCTGTGGCCAGGTGC	2038
Oy	2032	TTTTTCCATTAACAGGGGTGTTGTGTGTGTGGGTGTG	2069
Db	2039	TTTTTCCAGCCACAGGGTGTGTGTGTGTGAGCTGTGTGTGTG	2076

RESULT 7
 US-07-668-648-1
 ; Sequence 1, Application US/07668648
 ; Patent No. 5416192
 ; GENERAL INFORMATION:
 ; APPLICANT: Shoyab, Mohammed
 ; APPLICANT: Plozman, Gregory D.
 ; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
 ; TITLE OF INVENTION: MODULATING PROTEINS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/668,648
 ; FILING DATE: 19910819
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 5624-161-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)/90-9090

QY 1513 TCTGCCACCTGCCACCTTCTGCGCCGCTGACCTGAGTGGTGAAGACGTGGAG 1572
DB 1495 TGTGTCCACCTTCCATGAGCCTGACCTTGGCTTAAGTTGG-----GAATGTGAA 1548
QY 1573 TGTGGGGAAGACACTTTCGATGATTAACAGACCTGCTCCGAGACAACCCAGAGGC 1632
DB 1549 TGTGGGCGCGGACATTTGTGCGCATGATTAACAGACCTGCTGTTGTAAGACAGCCAGAGAGC 1608
QY 1633 TGGGCGCTGTCCTCCACGCGCCGCTGCTGTTGTGATGCGGCGCACCTGCTGCT 1692
DB 1609 TGGGCGCTGTCCTCCATGTAAGAGGTGCTGCTGTAAGATGAGAGCTGCTGCTGCT 1668
QY 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
DB 1669 ATTGGCTTCCACTGTCACGCAAGGACCAAGTGTGCTGCGGAAGAACCCCTGCTGCT 1728
QY 1753 GACGCGCTTGTGAGGACCGCTTGTGAGACAGCTGCTG 1791
DB 1729 GACATACCTTTGAGGATCCAGCCCAAGACCGCTACTG 1767

RESULT 9
US-08-431-333-1
; Sequence 1, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plozman, Gregory D.
; TITLE OF INVENTION: EPIHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1767 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1767
US-08-431-333-1
Query Match 54.5%; Score 1142.6; DB 2: Length 1767;
Best Local Similarity 78.9%; Pred. No. 1,9e-277;
Matches 1403; Conservative 0; Mismatches 364; Indels 12; Gaps 3;

QY 13 ATGTGAGACCTGGTGAAGTGGTGGCTTAAACAGAGGGGTGGTGGTGAAGCGGGTGC 72
DB 1 ATGTGAGTCTGGTGAAGTGGTGGCTTAAAGTGGTGAAGCGGGTGGTGGTGAAGCGGGTGC 60
QY 73 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
DB 61 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 133 TGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
DB 121 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 193 TGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
DB 181 TGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 253 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
DB 241 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 313 CCGGGGCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 372
DB 301 CCGGGGCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 358
QY 373 GTGGGTGCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 432
DB 359 -TGGGTGCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 417
QY 433 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
DB 418 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 493 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
DB 478 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
QY 553 CCCAGCGGACCCAGCCCTGCGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 612
DB 538 CCCAGCGGACCCAGCCCTGCGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 597
QY 613 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
DB 598 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
QY 673 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
DB 658 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
QY 733 TCCGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
DB 718 TCCGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 793 CTCTCCAGGAGAAAGCTTACAGGAGCTTCTTACAGGAGCTTCTTACAGGAGCTTCTTAC 852
DB 778 ATATCCAGGAGAAAGCTTACAGGAGCTTCTTACAGGAGCTTCTTACAGGAGCTTCTTAC 834
QY 853 GATGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
DB 835 GATGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 913 TCGGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
DB 895 ACTGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
QY 973 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
DB 955 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
QY 1033 CAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1092
DB 1015 CAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074

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QY 1093 AAGAGATGTCCTGATATATGACAGAGCTCTCCCTCCGATACCTGCTGCCAA 1152
D 1075 AAGATGATGTCCTGATGATGACTGATGACTGCTCTCTTAAACAATACCTGCTGCAGA 1134
QY 1153 CTACGCTGCGGAGATGGGGGCTGTCGAATCCAGAGGCTGTGGGCTGGAGCAAC 1212
D 1135 CTGACTTCTGGGAGATGGGGGCTGCTGCTCCATCCAGAGGCTGTGCTGCTTAAGACCC 1194
QY 1213 CAGCAGCTGCGCCCGACGATACAGTGTGTAGCTGAGGGGCACTGACGAGCAAGC 1272
D 1195 CAGATGCTGCGCTCAGAGGCTTCAATGATGATGAGGGGCTACTGTGACAGAGGAGAGC 1254
QY 1273 GAGATGCTGCGCTGAGAGAGATGCTGCGCCCGCGGCTCTTATCCACCCAGA 1332
D 1255 AGAATGCTGCGCTGAGAGAGATGCTGCGCCCGAGACAACCTGCTCCATCATGATGA 1314
QY 1333 GACATGCGCTGAGACAGACACAGTGCCTGCGGGGAGAACTGCTGCCCGGAGCCAG 1392
D 1315 GATATGCTGAGACAGACATACAGCTGCGCCAGTAGGAGCAATGCTGCCAAGCCCTG 1374
QY 1393 GGTGGAGCTGGGCTGCTGCGCAGTTCGCCCATGCTGTGCTGCGAGGATGCGCAGAC 1452
D 1375 AAGGAGATGGGCTGCTGCGCAGTTCGCCCATGCTGTGCTGAGAGACCGGACAGAC 1434
QY 1453 TGTGCTGCGGCTGCTGACACTGACAGCTGAAAGCTCATCTGCGAGAGAGAGTGTG 1512
D 1435 TGTGCTGCGGCTGCTGACACTGACAGCTGAAAGCTCATCTGCGAGAGAGATGCTG 1494
QY 1513 TGTGCTGCGGCTGCTGACACTGCTGCGCAGTTCGCCCATGCTGTGCTGCGAGGCTG 1572
D 1495 TGTGCTGCGGCTGCTGACACTGACACTTGTGCTGCTGAGTTGG-----GAAATGGAA 1548
QY 1573 TGTGGGGAAGGACACTTGTGCGATGATTAACAGACAGCTGCTGCGCAGACAGCAGG 1632
D 1549 TGTGCTGCGGACACTTGTGCGATGATTAACAGACAGCTGCTGCTGTAAGACAGCAAG 1608
QY 1633 TGGGCTGCTGCTGCTGCGCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1692
D 1609 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1668
QY 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1752
D 1669 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728
QY 1733 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
D 1729 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1767

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RESULT 10
PCT-US91-02321-1
Sequence 1, Application PC/TUS9102321

```

: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: APPLICANT: Plovman, Gregory D.
: TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bristol-Myers Squibb Company
: STREET: 3005 First Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/02321
: FILING DATE: 19910403

```

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: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Poor, Brian W.
: REGISTRATION NUMBER: 32,928
: REFERENCE/DOCKET NUMBER: ON0071A-PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)728-4800
: TELEFAX: (206)448-4775
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1767 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Rat
: TISSUE TYPE: Kidney
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1767
: PCT-US91-02321-1

Query Match 54.5%, Score 1142.6; DB 5; Length 1767;
Best Local Similarity 78.9%; Pred. No. 1.9e-277;
Matches 1403; Conservative 0; Mismatches 364; Indels 12; Gaps 3;

QY 13 ATGTGAGCCCTGGTGTGAGGCTGGGCTGCTTAACAGAGGCTGTGGGCTGGAAGCGGCTG 72
D 1 ATGTGATCTCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 73 CCAGATGCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
D 61 CCAGATGCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 133 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
D 121 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 193 TGGCAGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
D 181 TGGCAGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 253 TCCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
D 241 TCCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 313 CGGGCTTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
D 301 CGGGCTTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358
QY 373 GTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
D 359 -TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
QY 433 GTTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
D 418 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
QY 493 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
D 478 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537
QY 553 CCCACGGGACCCACCCCTGCGCAAGAGCTGCTGCGCAGAGGCTGCGCAAGAGGCTGCTG 612
D 538 CCCACGGGACCCACCCCTTACTTAAGAAATTCCTCCGCAAGAGGCTGCGCAAGAGGCTG 597
QY 613 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
D 598 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 673 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732

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ORIGINAL SOURCE:
ORGANISM: Mus musculus
TISSUE TYPE: Kidney
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
US-08-429-998-5

Query Match 52.9%; Score 1107.4; DB 2: Length 1767;
Best Local Similarity 77.6%; Pred. No. 1.3e-268;
Matches 1381; Conservative 0; Mismatches 386; Indels 12; Gaps 3;

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1 ATGTGGGTCTGTAGTGGCTGGCTTCCGCGAGGGGTGGTGGTGGTGGTGGTGGT 60
73 CCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
61 CCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
133 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
121 TGTGTAACCTCTGTGAGACATGGCTGATGATGATGATGATGATGATGATGATGAT 180
193 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
181 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
253 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
241 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
313 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
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373 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
358 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
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538 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
613 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
598 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
673 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
658 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
733 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 792
718 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
793 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852
778 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
853 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
835 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
913 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972

895 ACTGGGGCTGGGGCTGCTCTCTCCATTTTCCCAAGGCCCTGGTGGTGGATACATTCAT 954
973 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1032
955 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1014
1033 CAGGTGCTGTGATGAGGAAGGCCCGACCTACCTGACCTGACGACCAAGCCCTTG 1092
1015 CAAGTATCCCTGATGAGGAAGGTATGATGATGATGATGATGATGATGATGATGAT 1074
1093 AAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
1075 AAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134
1153 CTGATGCTGGGGGATGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
1135 CTGATGCTGGGGGATGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
1213 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
1195 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
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1255 ACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
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1315 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
1393 GGTGGAGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
1375 AAGGGAAGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
1453 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1512
1435 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1494
1513 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1572
1495 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1548
1573 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1632
1549 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1608
1633 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1692
1609 TGTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1668
1693 GCTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1752
1669 GCTGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1728
1753 GACGCTCCCGGGGCTTTAGCTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCAC 1792
1729 GACATGCTTTTGAAGGATCCGCTCCCAAGACCGCTACTG 1767

RESULT 13
US-08-431-333-5
Sequence 5, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plozman, Gregory D.
TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
NUMBER OF SEQUENCES: 12
MODULATING PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 12:51:09 ; Search time 2706 Seconds
(without alignments)
12538.634 Million cell updates/sec

Title: US-08-991-862-16
2095
Perfect score: 1 cgcgcagcagcaccatgttgac.....ataaagttgtcacttctt 2095
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1209.6	57.7	2145	11	AK013678 Mus muscu
2	1208	57.7	2170	11	AK018744 Mus muscu
3	966.2	46.1	986	9	AL548072 AL548072
4	949.2	45.3	1089	13	BM54590 AGENCOURT
5	943.6	45.0	1033	9	AL551350 AL551350
6	928.4	44.3	1010	9	AL542702 AL542702

c	7	918	43.8	1018	9	AL572883	AL572883
c	8	914	43.6	932	9	AL561424	AL561424
c	9	904	43.2	996	9	AL582634	AL582634
c	10	901.8	43.0	934	9	AL541798	AL541798
c	11	880.6	42.0	920	9	AL552664	AL552664
c	12	873.8	41.7	942	9	AL542659	AL542659
c	13	870.4	41.5	894	9	AL557765	AL557765
c	14	854.4	40.8	888	9	AL544054	AL544054
c	15	849	40.5	991	13	BM68251	BM68251
c	16	848.6	40.5	919	14	BM78155	BM78155
c	17	843.8	40.3	930	14	BM81528	BM81528
c	18	841.8	40.2	1004	14	BM807165	BM807165
c	19	837.6	40.0	950	14	BM36810	BM36810
c	20	834.2	39.8	1126	13	BM544984	BM544984
c	21	832.4	39.7	979	14	BM19561	BM19561
c	22	831	39.7	928	14	BM683772	BM683772
c	23	828.2	39.5	881	14	BM18213	BM18213
c	24	822.6	39.3	1035	14	BM061031	BM061031
c	25	821.6	39.2	995	14	BM06302	BM06302
c	26	820.6	39.2	865	9	AL551474	AL551474
c	27	819.8	39.1	936	14	BM925345	BM925345
c	28	819.2	39.1	924	14	BM06910	BM06910
c	29	819.2	39.1	1126	13	BM550274	BM550274
c	30	817.8	39.0	900	9	AL574944	AL574944
c	31	816.8	39.0	1062	14	BM808271	BM808271
c	32	815.6	38.9	865	9	AL554194	AL554194
c	33	813.4	38.8	855	13	BM009189	BM009189
c	34	812	38.8	895	14	BM090375	BM090375
c	35	811	38.7	1033	14	BM058416	BM058416
c	36	810.8	38.7	1004	13	BM562443	BM562443
c	37	807.4	38.5	948	14	BM958748	BM958748
c	38	806	38.5	923	14	BM650063	BM650063
c	39	804.8	38.4	929	14	BM955902	BM955902
c	40	804.8	38.4	975	14	BM960488	BM960488
c	41	804.8	38.4	1047	14	BM052452	BM052452
c	42	803.2	38.3	938	14	BM920068	BM920068
c	43	801.8	38.3	1007	14	BM060872	BM060872
c	44	800.8	38.2	1026	13	BM554117	BM554117
c	45	799.2	38.1	1031	14	BM061852	BM061852

ALIGNMENTS

RESULT 1	AK013678
LOCUS	AK013678
DEFINITION	Mus musculus adult male hippocampus cDNA, RIKEN full-length
ACCESSION	AK013678
VERSION	AK013678.1 GI:12851131
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain: c57BL/6J) adult male hippocampus cDNA to mRNA, clone: 2900053623.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS	Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
TITLE	Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	20499374
MEDLINE	11042159
PUBMED	3
REFERENCE	

Db 391 G---ATTAACCCCTTGGGTCTGTCAGTCTCCGAGGAGCCAGTTTAAATCTCTGACTCT 447
 Oy 421 TCCAGTGTCTGTATGTGATGATGCTCTGAGGGGTGCTGCCCAATGCCCAAGGCTTGC 480
 Db 448 GCCACTGCTGCTATATGTGTGATGCTCTGAGGGATGTTGTCTCCATGCCCAAGGCTTGC 507
 Oy 481 TGTGTGAAGACAGAGGTGATGCTCTGAGGGATGTTGTCTCCATGCCCAATGCCCAAGGCTTGC 540
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 Oy 541 CCGTGTATAC 600
 Db 568 CCAATGGGTTTAC 627
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 Db 628 AACAGGACAGTGTCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687
 Oy 661 GATGTTTCTACTGCTGTGTGAGTGTCCAGTGTGAGGATGATGATGATGATGATGATGATGATG 720
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 Oy 721 GCCACTGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
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 Oy 841 CACACATGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 Db 865 TACCCATGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 924
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 Db 925 TGCCTGTCTACAGTGTGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 984
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 Oy 1021 CAGGGGCCCCACAGTGTGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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 Db 1105 CCACAAGCCCTTGAAGAGATGTCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1164
 Oy 1141 ACCTGTGTCTACAGTGTGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 Db 1165 ACCTGTGTCTACAGTGTGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1224
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 Oy 1441 GATCGGAGGAGTGTGTCCTGCGGCGTGTACACGTCGAAAGGCTGATGATGATGATGATGATGATGATG 1500

Db 1465 GACCGGACGATCTGTGTCCTGCGGCGGTACACCTGCATGTGAAGGCGAGGACTGTGAG 1524
 Oy 1501 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 1560
 Db 1525 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 1580
 Oy 1561 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 1620
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 Oy 1913 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 1971
 Db 1939 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 1998
 Oy 1972 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 2031
 Db 1999 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 2058
 Oy 2032 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 2096
 Db 2059 AAGAAAGTGTCTCTGCGGAGGCTGACACCTGCTGAGGCGGATGATGATGATGATGATGATGATGATG 2106

RESULT 2
 AK018744
 LOCUS 2170 bp mRNA linear HTC 19-JAN-2002
 DEFINITION Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012H06:granulin, full insert sequence.
 ACCESSION AK018744
 VERSION AK018744.1 GI:12858615
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:0610012H06.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL MEDLINE 99279253
 PUBMED 10349636
 TITLES
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL MEDLINE 20499374
 PUBMED 11042159
 REFERENCES
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Db 416 G---AATACCCCTTGGGTCTGTCTGACAGTCTCCGGGAGCCAGTTTGAATGCTCTGACTCT 472
OY 421 TCCAGTGGCTGTGTATGGTCATGCTCTGGGGGTCGCCCAATGGCCCAAGGGTCTGC 480
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Db 533 TGGCTGAAGACAGAGTGTGATGCTTCCCATGGGGCTCGTGTACCTGGTTCAACA 592
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OY 661 GATGTTTCACTGCTGTGAGCTGCCAGTGGGAGTATGGCTGTGCCCAATGCCCAAC 720
Db 713 GATGATTTTCACTGCTGTGAGTACCACAGTGGAGTATGGTGTGATGCCAATGCCCAAT 772
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Db 773 GCCATGTGCTGTCCACACACCTGCACTGCTGCCCCAGACACTGTATGTGACTGTATC 832
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Db 890 TACCCAGTGAAGAGGTGAAGTGCAGATGAGAGTGAAGTGGCCCTGAAGGATATATCTGC 949
OY 901 TGGCTGTACAGTGGGGGCTGTGGGCTGTGCTCTTTTACCAGGCTGTGTGCTGTGAG 960
Db 950 TGGCGCTCAACACTGTGGGCTGTGGCTGTGCTCAATTTGCCAAGGCGCTGTGTGAG 1009
OY 961 GACCAATACAGTGTGCTGCCGGGGTTTACGTGACACGACGAGAGAGGTTACTCTGTGA 1020
Db 1010 GATCACAATTCATGTCTGCCCGGAGGGTTTCAATGTACACAGAGAGAAAGAACTGTGGA 1069
OY 1021 CAGGGGCCCCACAGAGTGGCTGTGATGAGAGAGCCCCAGCTCAGCTCAGCTGCCAGAC 1080
Db 1070 ATGGATATCTCCCAATGATGATGAGAGATGATACCCCTCCGCTGCCAGAC 1129
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OY 1141 ACCTGTGCACTCAAGTGTGGGAGTGGGGTGTGCTCAATGCCAGAGGGTGTCTGC 1200
Db 1190 ACCTGTGCAACTCAATGTGGGAGTGGGGTGTGCTCAATGCCAGAGGGTGTCTGC 1249
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Db 1250 TGGTGAAGACACAGCAGTGTGCTGCCAGGGCTTACAGATGTGTGGGTCAAGGGGTACTGT 1309
OY 1261 CAGCGAGAGAGCAGATGTGGCTGTGAGTGTGAAGAGATGTCTCCCGCGGTTCTTGA 1320
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OY 1321 TCCGACCCAGAGATGCTGTGACACACACAGCAGTGGCCGGGAGGAGACCTGC 1380
Db 1370 CTTCGAATTTGAGATATCGTTGTGACACACATACCAAGCTGCCAGTAGGGCAACCTGC 1429
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Db 1430 TGGCCGAGCTCAAGGGAAGTGTGGCTGTGTGCAAGTGTGCCCATGTGTGTGTGAG 1489
OY 1441 GATTCGACAGCAGTGTGCTGGCTGTGACACTGCAACGTGAAGGCTGCATCTGCGAG 1500

Db 1490 GACCGGACAGCACTGTTGCCCGGGGTACACCTGCAATGTGAAGGAGGACCTGTGAG 1549
OY 1501 AAGAAAGTGTCTCTGCGACAGCTGCACTTCTGCGCCCGTGAAGCCCTACAGTGGTGTG 1560
Db 1550 AAGATGTGATTTTATCCAGCTCCCGTGTCTCTTACCTGTGGCCCTTAAGTTGG----- 1605
OY 1561 AAGAGCTGAGTGTGGGAGAGACATTTCTGCCATGATTAACAGACCTGTGCCAGAC 1620
Db 1606 --GAATGTGAGTGTGAGAAAGGCAATTTCTGCCATGATTAACAGACCTGTGTAAAGAC 1663
OY 1621 AACCGACAGGCTGGGCTGTCTCTTCTTACGCCAGGGGCTGTGTGTGATGTGGCCG 1680
Db 1664 AGTCAAGAGTGTGGGCTGTCTCTCTCTTCACTTAAAGGTTGTGTGATGAGTGTGACGT 1723
OY 1681 CACTGTGTCTGTGAGTCTCCGTCGCGACGAGAGGGTACCAAGTGTGTGCGCAGGGAG 1740
Db 1724 CACTGTGTGCGCGGTGTCTTCACTGTTCAGCCAGGGGAAACAAAGTGTGTGCCAAAGAG 1783
OY 1741 GCCCGCGCTGGGAGCGCCCTTGTGAGGAGCCAGACCTTGAGACAGTGTGTGAGGAGAC 1800
Db 1784 ATTCCTGTGCGGACATGTTTGTGAGGATCCGTCACAAAGCCGCTACTGTAAAGAGG 1843
OY 1801 GTACTGA-----GACTGTGAGCCCTGTGGAGACCCCACTCGGAGGTTGCTGTCTC 1853
Db 1844 GTTACAGACTTAAAGAACTCACAGTCTGGAACCTGTGCGAGAGTACCCACTATCTC 1903
OY 1854 AGGCTTCCCTAGCAGCTCCCTTACCAAAATTCCTCCGAGACCCATTTCTGAG -CTCCCC 1912
Db 1904 AGGCTTCCCTAGGCGCTCTCTTCAAGCTGTCCCGGCTACTCATCTGAGTCAACCT 1963
OY 1913 ATCACAATGGAGTGGGCGCTCAATCTAAGGCTTCCCTGTGAGAGAGGGGTTGAGG- 1971
Db 1964 ATCACAATGGAGTGGAGCTCAAACTAAACCTTCTTTATGAGAAAGAGGCTGTGGG 2023
OY 1972 CAAAAGCCCTTACAAAGTCCATCCCTCCCGTTTCAATGAGACCTGTGGCCAGTGTG 2031
Db 2024 CAAAAGCCCTTACAAAGTCTTCCGTTTCTGTGGACCTGTGTGGCCAGTGTG 2083
OY 2032 TTTTCCCTATCACAGGAGGTGTGTGTGTGGGTGTG 2069
Db 2084 TCTTCCGAGCCACAGGTGTCTGTGAGCTTGTGCTGTG 2121

RESULT 3
AL548072 986 bp mRNA linear EST 16-FEB-2001
LOCUS AL548072 L1_NFL006.Pl2 Homo sapiens cDNA clone CS0D1034Y17 5
DEFINITION AL548072 L1_NFL006.Pl2 Homo sapiens cDNA clone CS0D1034Y17 5
ACCESSION AL548072
VERSION AL548072.1 GI:12882738
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 986)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. 986
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/db_xref="taxon:9606"
/clone="CS0D1034Y17"
/clone_lib="L1_NFL006.Pl2"
/issue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 168 a 323 c 290 g 203 t 2 others
ORIGIN

Query Match 46.1%; Score 966.2; DB 9; Length 986;
Best Local Similarity 99.6%; Pred. No. 2.9e-222;

Matches 977; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

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OY 1 CGCAGGACGACCATGTGACCCCTGGTGAAGTGGTGGCTTAAACAGACAGGGCTGGGCT 60
DB 6 CGCAGGACGACCATGTGACCCCTGGTGAAGTGGTGGCTTAAACAGACAGGGCTGGGCT 65
OY 61 GGAAGCGGCTGCGCCAGATGTCATTTGCGCTTGGCTGCTGGACCCCGAGAGA 120
DB 66 GGAAGCGGCTGCGCCAGATGTCATTTGCGCTTGGCTGCTGGACCCCGAGAGA 125
OY 121 GCCAGCTACAGTGTGCGCCCTTCCGCAATGGCCCAACACTGAGCAGGCAT 180
DB 126 GCCAGCTACAGTGTGCGCCCTTCCGCAATGGCCCAACACTGAGCAGGCAT 185
OY 181 CTGGGTGGCCCTGCGCAGGTGATGATGCCACTGCTGCGGCGACTGCTGATCTTTAC 240
DB 186 CTGGGTGGCCCTGCGCAGGTGATGATGCCACTGCTGCGGCGACTGCTGATCTTTAC 245
OY 241 GTCTCAGGACCTTCAAGTTGTCCTTCCAGAGCGCTGGCATGGCGGATGGCCAT 300
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OY 301 CACTGCTGCGCCAGGGGCTTCCACTGACATGACAGCGGGCGATCCGCTTCCAAAGATCA 360
DB 306 CACTGCTGCGCCAGGGGCTTCCACTGACATGACAGCGGGCGATCCGCTTCCAAAGATCA 365
OY 361 GGTAAACAATCCGTTGGGTGCATTCAGTCCCTGATAGTCAATGACCCGAGACTTC 420
DB 366 GGTAAACAATCCGTTGGGTGCATTCAGTCCCTGATAGTCAATGACCCGAGACTTC 425
OY 421 TCCAGTGTGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 480
DB 426 TCCAGTGTGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 485
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OY 721 GCCACCTGCTGTCCGATACCTGATGCTGCTGCCCAAGACATGTTGTGACCTGATC 780
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OY 781 CAGACTAAGTGTCTTCCAGAGAAAGCTTACACAGGACTCTCTACTTAAGTGGCTGGC 840
DB 786 CAGACTAAGTGTCTTCCAGAGAAAGCTTACACAGGACTCTCTACTTAAGTGGCTGGC 845
OY 841 CACACAGTGGGATGTGAATGTGACATGAGGTGAGTGGCCAGATGGCTATACCTGC 900
DB 846 CACACAGTGGGATGTGAATGTGACATGAGGTGAGTGGCCAGATGGCTATACCTGC 905

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OY 901 TCCCTTACACTCGGGGCGCTGGGCTGCTGCCCTTTTACCAAGCTGTGCTGAG 960
DB 906 TCCCTTACACTCGGGGCGCTGGGCTGCTGCCCTTTTACCAAGCTGTGCTGAG 965
OY 961 GACCAATACACTGCTGTGCC 981
DB 966 GACCAATACACTGCTGTGCC 985

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RESULT 4
BM554590 1089 bp mRNA linear EST 20-FEB-2002

LOCUS AGENCOURT_6580965 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469522

DEFINITION 5' mRNA sequence.

ACCESSION BM554590

VERSION BM554590.1 GI:18794315

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

TITLE NIH-MGC http://mgc.nhl.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaab3-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution Information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LNCM1974 row: n column: 19

High quality sequence start: 4

High quality sequence stop: 684.

Location/Qualifiers

1..1089

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="5469522"

/clone_id="NIH_MGC_41"

/tissue_type="amelanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

BASE COUNT 189 a 347 c 332 g 219 t 2 others
ORIGIN

Query Match 45.3%; Score 949.2; DB 13; Length 1089;
Best Local Similarity 96.3%; Pred. No. 3.8e-218;

Matches 1013; Conservative 0; Mismatches 35; Indels 4; Gaps 4;

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OY 1 CGCAGGACGACCATGTGACCCCTGGTGAAGTGGTGGCTTAAACAGACAGGGCTGGGCT 60
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OY 61 GGAACGGGCTGCGCCAGATGTCATTTGCGCTTGGCTGCTGGACCCCGAGAGA 120
DB 90 GGAACGGGCTGCGCCAGATGTCATTTGCGCTTGGCTGCTGGACCCCGAGAGA 149
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QY 181 CTGGTGGCCCTGCGCCAGTTGATGCTCTGTCGGGCGCAGTCTGATCTTTACC 240
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Db 210 CTGGAGGGGCGCCCTGCGCCAGTTGATGCTCTGTCGGGCGCAGTCTGATCTTTACC 269
QY 241 GTCTCAGGAGCTTCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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Db 270 GTCTCAGGAGCTTCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329
QY 301 CACTGCTGCCACAGGGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Db 330 CACTGCTGCCACAGGGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
QY 361 GGTAACTACCTCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 390 GGTAACTACCTCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
QY 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Db 450 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
QY 481 TGGTGAAGACAGGGTGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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Db 510 TGGTGAAGACAGGGTGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559
QY 541 CGCTGATACACACCCAGGGGACCCACCCCTGGGCAAGAGTCTGCTGCTGCTGCTGCT 600
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Db 750 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
QY 781 CAGAGTAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
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Db 810 CAGAGTAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
QY 841 CACACAGT-GGGGATGTGAATGTGACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 899
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Db 869 CACACAGTGGGGGATGTGAATGTGACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 928
QY 900 CTGCGCTTACAGTC-GGGGGCTGGGGCTGCTGCTGCTTTCACAGGCTGTGTGCTG 958
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Db 929 CTGCGCTTACAGTCGGGGGCTGGGGCTGCTGCTGCTTTCACAGGCTGTGTGCTG 988
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Db 989 AGGACACATACAGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
QY 1018 GAACAGGGGCGCCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
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RESULT 5
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LOCUS AL551350 LTR1.NFL006.Pl2 Homo sapiens cDNA clone CSDD1064Y14.5
DEFINITION prime, mRNA sequence.
ACCESSION AL551350
VERSION AL551350.1 GI:12889213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1033)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/db_xref="taxon:9606"
/clone="CSDD1064Y14"
/clone_1lb="LTR.NFL006.Pl2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 176 a 334 c 308 g 214 t 1 others

ORIGIN

Query Match 45.0%; Score 943.6; DB 9; Length 1033;
Best Local Similarity 98.6%; Pred. No. 8,4e-217;
Matches 982; Conservative 1; Mismatches 10; Indels 3; Gaps 3;

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Db 98 GGAACGGGTGCCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
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Db 158 GCGAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 217
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Db 218 CTGGTGGCCCTGCGCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
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Db 278 GTCTCAGGAGCTTCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337
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Db 338 CACTGCTGCCACAGGGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
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OY 720 GCGCAGCTGCTGCTGCTGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
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Db 938 CTGCGCTTACAGTGGGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
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RESULT 6
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LOCUS AL542702 LTI_FL002_PL1 Homo sapiens cDNA clone CS0D011YC02 5 prime
DEFINITION AL542702 LTI_FL002_PL1 Homo sapiens cDNA clone CS0D011YC02 5 prime
ACCESSION AL542702
VERSION AL542702.1 GI:12875005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1010)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db_xref="taxon:9606"
/clone="CS0D011YC02"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetechn.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT 170 a 327 c 300 g 211 t 2 others
ORIGIN

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Query Match 44.3%; Score 928.4; DB 9; Length 1010;
Best Local Similarity 99.3%; Pred. No. 3.8e-213;
Matches 951; Conservative 2; Mismatches 3; Indels 2; Gaps 2;
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OY 121 GCGACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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Db 294 GTCCTAGGAGCTTCCAGTGGTGGCCCTTCCAGAGGCGGTGGCATGCGGGGATGGCAT 353
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Db 354 CACTGCTGCCACGCGGCTTCCAGTGGTGGCCCTTCCAGAGGCGGTGGCATGCGGGGAT 413
OY 361 GGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 414 GGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
OY 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 474 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
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Db 594 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
OY 601 AACAGGAGTGGCTTTCAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 654 AACAGGAGTGGCTTTCAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
OY 661 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 714 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
OY 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 774 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
OY 781 CAGAGTAAAGTGGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 833 CAGAGTAAAGTGGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 892
OY 841 CACACAG-TGGGCGATGTGAATGTGACATGAGGTGAGTGGCCAGATGCTATACCTG 899
Db 893 CACACAGTGGGCGATGTGAATGTGACATGAGGTGAGTGGCCAGATGCTATACCTG 952
OY 900 CTGCGCTTACAGTGGGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
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RESULT 7
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LOCUS AL572883 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1034YC17 3
DEFINITION AL572883 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1034YC17 3
ACCESSION AL572883
VERSION AL572883.1 GI:12931579
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 1018
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS01034YCI17"
/clone_1ib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site: 1. NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 199 a 306 c 331 g 172 t 10 others
ORIGIN

Query Match 43.8%; Score 918; DB 9; Length 1018;
Best Local Similarity 96.9%; Pred. No. 1.2e-210;
Matches 980; Conservative 7; Mismatches 19; Indels 5; Gaps 5;

QY 1055 CCCCACTACCTCAGCTCCAGCCACCCACCAAGCTTGAAGAGAGTCCCTGTATATA 1114
DB 1018 CCCCACTACCTCAGCTCCAGCCACCCACCAAGCTTGAAGAGAGTCCCTGTATATA 959
QY 1115 ATGTACAGAGCTGTCCCTCCCTCCGATACCTGCTGCAACTCAGCTGGGAGTGGGGCT 1174
DB 958 ATGTACAGAGCTGTCCCTCCCTCCGATACCTGCTGCAACTCAGCTGGGAGTGGGGCT 899
QY 1175 GCTGTCCATCCAGAGAGCTGTGTCTGCTGCGACACACGACTGCTGCCACGAT 1234
DB 898 GCTGTCCATCCAGAGAGCTGTGTCTGCTGCGACACACGACTGCTGCCACGAGGCT 839
QY 1235 ACACGTGTGAGTGAAGGGGAGTGCAGAGGAGGAGGAGTGCAGGAGTGCAGTGA 1294
DB 838 ACACGTGTGAGTGAAGGGGAGTGCAGAGGAGGAGGAGTGCAGTGAAGTGCAGTGA 779
QY 1295 AGATG-CCTGCCCCCGCGGCTTATCCACCCAGAGACATCGCTGTGACACGAC 1353
DB 778 AGATGCGCTCCCGCGGGGCTTATCCACCCAGAGACATCGCTGTGACACGAC 719
QY 1354 A-CCAGCTCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1412
DB 718 ACCCACTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
QY 1413 CCAGTTGCCCATGCTGTGTGCTGCGAGATCGCAGACATGCTGCCCGGCTGGCTAC 1472
DB 658 CCAGTTGCCCATGCTGTGTGCTGCGAGATCGCAGACATGCTGCCCGGCTGGCTAC 599
QY 1473 CTGCAACGTGAAGGCTGATCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1532
DB 598 CTGCAACGTGAAGGCTGATCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
QY 1533 CTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1592
DB 538 CTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
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DB 478 CCATGATTAACGACGCTGCTGCCGAGCAACGACAGGCTGGGGCTGTGCTTACCG 419
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DB 418 CCAAGGCGCTGTGTGTGCTGATGCGGCGCACATGCTGTGCTGTGCTGTGCTGCGCAG 359
QY 1713 CAGGGGTACCAAGTGTGTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1772
DB 358 CAGGGGTACCAAGTGTGTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 299
QY 1773 AGCCTTGAGACAGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1832
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DB 238 CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 179
QY 1893 GACCCATTTGAGCTCCCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1952
DB 178 GACCCATTTGAGCTCCCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 120
QY 1953 TGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2011
DB 119 TGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
QY 2012 TGGACCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2061
DB 59 TGGACCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9

RESULT 8
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LOCUS
DEFINITION AL561424 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL007Y12 5
ACCESSION AL561424
VERSION AL561424.1 GI:12908842
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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Location/Qualifiers
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/clone="CS0DL007Y12"
/clone_1ib="LTI_NFL010_BC2"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/note="Vector: pCMVSPORT 6; Site: 1. NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 160 a 305 c 277 g 189 t 1 others
ORIGIN

Query Match 43.6%; Score 914; DB 9; Length 932;

Best Local Similarity 99.7%; Pred. No. 1.le-209;
Matches 925; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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OY 1 GCAGGACACACCATGAGGACCTGGGAGCTGGGAGCTTAACAGACAGAGGAGGCT 60
DB 6 CCAGGACACACCATGAGGACCTGGGAGCTGGGAGCTTAACAGACAGAGGAGGCT 65
OY 61 GAGAGCGGCTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 66 GAGAGCGGCTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 125
OY 121 GCGAGCTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 126 GCGAGCTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
OY 181 CTGGGAGGCGGCTGGCCAGGTTGATGATGATGATGATGATGATGATGATGATGAT 240
DB 186 CTGGGAGGCGGCTGGCCAGGTTGATGATGATGATGATGATGATGATGATGATGAT 245
OY 241 GTCTGAGGACCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 246 GTCTGAGGACCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
OY 301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 306 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
OY 361 GGTACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 366 GGTACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
OY 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 426 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
OY 481 TCTGTGAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 540
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OY 541 CCGTGCATACACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB 546 CCGTGCATACACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 605
OY 601 AACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 606 AACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 665
OY 661 GATGGTTCACAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 666 GATGGTTCACAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 725
OY 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 726 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
OY 781 CAGAGTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 786 CAGAGTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
OY 841 CACACAGTGGGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 846 CACACAGTGGGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 904
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RESULT 9
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LOCUS AL582634 LTI_NFL010.BC2 Homo sapiens cDNA clone CS0DL007YF12 3
DEFINITION prime, mRNA sequence.

ACCESSION AL582634
VERSION AL582634.1 GI:12950809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Li, W.B., Gruber, C., Jessup, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 199 a 299 c 320 g 171 t 7 others
ORIGIN

Query Match 43.2%; Score 904; DB 9; Length 996;
Best Local Similarity 96.9%; Pred. No. 2.9e-207;

Matches 957; Conservative 5; Mismatches 22; Indels 4; Gaps 4;

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DB 996 AGCTGCCAGACCCCAAGCCTTGAAGAGATGTCCTGATGATGATGATGATGAT 937
OY 1129 CCGTCTCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
DB 936 CCGTCTCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
OY 1189 GAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248
DB 877 GAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
OY 1249 GAGGGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1308
DB 817 GAGGGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759
OY 1309 CCGGCTTCTTATCCACCCCAAGACATCGGCTGTGACACAGACAGCAGTGG 1368
DB 758 CCGGCTTCTTATCCACCCCAAGACATCGGCTGTGACACAGACAGCAGTGG 699
OY 1369 GCGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
DB 698 GCGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
OY 1429 GTGTCTGCGAGAGATGCGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1488
DB 638 GTGTCTGCGAGAGATGCGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 579
OY 1489 CGATCTGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
DB 578 CGATCTGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
OY 1549 CACGTGGGTGTGAAGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1608

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Db	Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	518	CACGCGGGTGTGAAGAGACTGGATGTGGGAGAGACACTTCTGCAATGATTAACAGACC	459						
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Db	458	TGCTGCCAGAGACAAACCGACAGGGCTGGGCGTGTGTCTCCCTACGCCACGAGGGCTGTGTTGT	399						
Qy	1669	GCTGATGCGGGCGCACTGTGTGTCCTGTGGCTTCCGCTGCGACGAGGGGTACCAAGTGT	1728						
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Qy	1729	TTGGCGCAGGAGAGGCCCGCGCTGGGAGCCCGCTTTGAGGAGCCAGCCCTTGAAGACAGCTG	1788						
Db	338	TTGGCGCAGGAGAGGCCCGCGCTGGGAGCCCGCTTTGAGGAGCCAGCCCTTGAAGACAGCTG	279						
Qy	1789	CTGTGACGGGACAGTACTGTAAACACTGTGACAGCCCTTGAGACCCCACTGCGAGGGTGCCTC	1848						
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Db	218	TGCTTAGGCGCTCCCTTAGGACACTCCCGCTTACCAATTTCTCCCTGGAGCCCAATTCGAGCT	159						
Qy	1909	CCCCATCACCATGGAGGTGGGGGCTCAATCTAGAGCCCTTCCCTGTGAGAGAGGGGGTTG	1968						
Db	158	CCCCATCACCATGGAGGTGGGGGCTCAATCTAGAG - CTTTCCCTGTGAGAGAGGGGGTTG	100						
Qy	1969	AGGCAAAAGCC - CATTTACAGCTGTCACATCCCTCCCGCTTTCAGTGAACCCGTGGGCCAG	2027						
Db	99	TGGCAAAAGCCACATTAACAGCTGCCATCCCTCCCGCTTTCAGTGAACCCGTGGGCCAG	40						
Qy	2028	GTGCTTTTCCCTATCCACAGGGGTGTTT	2055						
Db	39	GTGCTTTTCCCTATCCACAGGGGTGTTT	12						
RESULT 10	AL541798								
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DEFINITION	AL541798	LTI_FL002_PL1	Homo sapiens	cdna	clone	CS0DE007Y118	5	prime	
ACCESSION	AL541798								
VERSION	AL541798.1	GI:12873213							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
TITLE	L1.W.B., Gruber, C., Jesssee, J. and Polayes, D.								
JOURNAL	Full-length cDNA libraries and normalization								
COMMENT	Unpublished (2001)								
FEATURES	Contact: Genoscope								
Source	Genoscope - Centre National de Sequencage								
	BP 191 91006 EVRY cedex - France								
	Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.								
	Location/Qualifiers								
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	/lab_host="DH10B"								
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	end enriched, double-stranded cdna was digested with Not I								
	and cloned into the Not I and Eco RV sites of the								
	pCMVSPORT 6 vector. Library was constructed with life								
	Technologies. Contact : Feng Liang life Technologies, a								
	division of Invitrogen 9800 Medical Center Drive Rockville								
	, Maryland 20850, USA Fax : (1) 301 610 8371 Email :								

BASE COUNT	170 a	295 c	284 g	180 t	5 others
Query Match	43.0%	Score 901.8;	DB 9;	Length 934;	
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641	ACGCAAGGATCCCGGATGCCCTGATGGTTCACCTGCTGTAGAGCTGCCCAATGGGAATAG	700			
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761	ACACTGTGTGATACCTGATCCAGAGTAATGCTCTCCAGAGGAAGAGTACACGAGAC	820			
181	ACACTGTGTGATACCTGATCCAGAGTAATGCTCTCCAGAGGAAGAGTACACGAGAC	240			
821	TCCCTACTAAGTGCCTGCGGCACACAGTGGGGATGTGAATGTGCATGAGAGTACGT	880			
241	TCCCTACTAAGTGCCTGCGGCACACAGTGGGGATGTGAATGTGCATGAGAGTACGT	300			
881	GCCCAAGATGGCTAATACCTGCTGCCGCTACAGTGGGGGCTGGGGCTGCTGCCCTTTA	940			
301	GCCCAAGATGGCTAATACCTGCTGCCGCTACAGTGGGGGCTGGGGCTGCTGCCCTTTA	360			
941	CCGAGGCTGTGCTGTGAGGACCAATACCTGCTGCTCCGCGGGGGTTTACGTGTGACA	1000			
361	CCGAGGCTGTGCTGTGAGGACCAATACCTGCTGCTCCGCGGGGGTTTACGTGTGACA	420			
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421	CGCAGAAGGATACCTGTGTGAACAGAGGGGCCCCACAGTGGCTTGTGATGAGAGAGGCCGAC	480			
1061	CTACACTACGCTGCGCAGACCAACAAGCTTGTGAAGAGATGTCCTGTGATTAATGTCA	1120			
481	CTACACTACGCTGCGCAGACCAACAAGCTTGTGAAGAGATGTCCTGTGATTAATGTCA	540			
1121	GCAGCTGTCCCTCTCCGATACCTGCTGCCAATCACTGCTGGGAGTGGGCTGCTGTC	1180			
541	GCAGCTGTCCCTCTCCGATACCTGCTGCCAATCACTGCTGGGAGTGGGCTGCTGTC	600			
1181	CAATCCCAAGGATGTCTGCTGTGGACACACAGACACTGTCGCCCGCAGATTAACGT	1240			
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1241	GTGTAGCTAGAGGGGAGTGTCAAGCAGAGAAAGAGATGCTGTGCTGATCTGAGAAAGATGC	1300			
661	GTGTAGCTAGAGGGGAGTGTCAAGCAGAGAAAGAGATGCTGTGCTGATCTGAGAAAGATGC	720			
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840	CCCATCTGTGTCTGCGAGAGATGCCAGACATGCTGCCCGGTGCTACACCTGCAACG	899			
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AL552664	AL552664	920 bp	mRNA	linear	EST: 16-FEB-2001
LOCUS	AL552664	920 bp	mRNA	linear	EST: 16-FEB-2001
DEFINITION	AL552664 LTL_NFL006.PL2 Homo sapiens cDNA clone CS0D1067YM23 5				
ACCESSION	AL552664				
VERSION	AL552664.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 920)				
TITLE	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr , Web : www.genoscope.cns.fr .				
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BASE COUNT	159 a 303 c 272 g 184 t				
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Query Match	42.0%; Score 880.6; DB 9; Length 920;				
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98	GGAAGCGGTCGCCAGATGATGATTCAGTTCTGCGCTTGCGCTGCTGACCCGAGAGA 157				
121	GCCAGCTACAGTGTGCTGCCGTCCCTTCTGGACAATAAGGCCACCAACTGACAGCAT 180				
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278	GTCTCAGGACTTCAGATTGCTGCCCTTCCAGAGGCCGTGGCATGGGGGATGGCAT 337				
301	CACGTCTGCCACGGGGGCTTCACATGACAGTGCAGACGGGCGATCTCGTCCAAAGTCA 360				
338	CACGTCTGCCACGGGGGCTTCACATGACAGTGCAGACGGGCGATCTCGTCCAAAGTCA 397				
361	GGAACCACTCCGTGGGTGCATCCAGTGCCTGTATGATGATGATGCAATGCCGACTTC 420				
398	GGAACCACTCCGTGGGTGCATCCAGTGCCTGTATGATGATGATGCAATGCCGACTTC 457				
421	TTCACGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480				

Query Match	Best Local Similarity	Score	DB	Length
41.7%	97.8%	873.8	DB 9	942
Pred. No. 5.5e-200;				

Matches	914;	Conservative	3;	Mismatches	15;	Indels	3;	Gaps	3;
QY	1011	TACCTGTGAACAGAGGGCCCCACAGAGTGCCCTGGAGTGAAGAGGCCACCTACCTCAG	1070						
Db	1	TACCTGTGAACAGAGGGCCCCACAGAGTGCCCTGGATGGAAGAGGCCACCTACCTCAG	60						
QY	1071	CTGCGCAGACCCCAACACCTTGAAGAGATGTCCTGATATATGTCAGACACTGTC	1130						
Db	61	CTGCGCAGACCCCAACACCTTGAAGAGATGTCCTGATATATGTCAGACACTGTC	120						
QY	1131	CTCTCCGATACCTGCTGCCAAGCTCAGCTGTGGGAGTGGGGGCTGTCTCAATCCAGA	1190						
Db	121	CTCTCCGATACCTGCTGCCAAGCTCAGCTGTGGGAGTGGGGGCTGTCTCAATCCAGA	180						
QY	1191	GAGTGTCTGCTGTGAGACACAGCAGCTGTGCCCCAGAGATACAGTGTAGCTGA	1250						
Db	181	GAGTGTCTGCTGTGAGACACAGCAGCTGTGCCCCAGAGATACAGTGTAGCTGA	240						
QY	1251	GGGGCAGTGTACAGAGAGAGAGATGTCGTGGACTGGAGAGATGTCCTGCCCGG	1310						
Db	241	GGGGCAGTGTACAGAGAGAGAGATGTCGTGGACTGGAGAGATGTCCTGCCCGG	300						
QY	1311	CGGTCCTTATCCACCCAGAGACATGGCTGTGACACAGACACAGCTGCCGGTGGG	1370						
Db	301	CGGTCCTTATCCACCCAGAGACATGGCTGTGACACAGACACAGCTGCCGGTGGG	360						
QY	1371	CGGAACCTGTGCTGCCAGAGAGAGAGTGGAGCTGGGCTGTGCCAGTGTGCCATGCTGT	1430						
Db	361	CGGAACCTGTGCTGCCAGAGAGAGAGTGGAGCTGGGCTGTGCCAGTGTGCCATGCTGT	420						
QY	1431	GTCCTGTGAGAGATGCCAGACACTGCTCCCGGCTGGCTACACCTGCAGAGTGAAGGCTCG	1490						
Db	421	GTCCTGTGAGAGATGCCAGACACTGCTCCCGGCTGGCTACACCTGCAGAGTGAAGGCTCG	480						
QY	1491	ATCTCGAGAGAGAGATGCTCTGTGCCAGACCTGACACCTTCTGCTGCCGCTACCTCA	1550						
Db	481	ATCTCGAGAGAGAGATGCTCTGTGCCAGACCTGACACCTTCTGCTGCCGCTACCTCA	540						
QY	1551	CTGGGCTGTGAAGAGAGCTGAGTGTGGGAGAGACACTTGTGCCATGATTAACAGAGCTG	1610						
Db	541	CTGGGCTGTGAAGAGAGCTGAGTGTGGGAGAGACACTTGTGCCATGATTAACAGAGCTG	600						
QY	1611	CTGCCAGAGACAG	1670						
Db	601	CTGCCAGAGACAG	660						
QY	1671	TGATCGAG	1730						
Db	661	TGATCGAG	720						
QY	1731	GCGCAG	1790						
Db	721	GCGCAG	779						
QY	1791	GTCAG	1850						
Db	780	GTCAG	839						
QY	1851	CTGAG	1910						
Db	840	CTGAG	898						
QY	1911	CCATCACCATGAG	1945						
Db	899	CCATCACCATGAG	932						

VERSION	AL557765.1	GI:12901692
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Li, W.B., Gruber, C., Jessee, J. and Polayes, D. (bases 1 to 894)	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.	
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	/sex="male"	
	/issue-type="T cells from T cell leukemia"	
	/note="Vector: pCMVSPORT 6, site 1. NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"	
BASE COUNT	157 a 294 c 263 g 179 t	1 others
ORIGIN		
Query Match	41.5%; Score 870.4; DB 9; Length 894;	
Best Local Similarity	99.5%; Pred. No. 3.6e-199;	
Matches	882; Conservative 1; Mismatches 2; Indels 1; Gaps 1;	
QY	1	CGCAGGAGACATGTGAGACCTGTGAGTGGGCTTAAAGAGAGGCTGTGGCT 60
Db	9	CGCAGGAGACATGTGAGACCTGTGAGTGGGCTTAAAGAGAGGCTGTGGCT 68
QY	61	GGAAGGGGAG 120
Db	69	GGAAGGGGAG 128
QY	121	GCGAGCTACAGCTCTGCGCTTGTGAGACAAATGAGCCACACAGAGAGAGAT 180
Db	129	GCGAGCTACAGCTCTGCGCTTGTGAGACAAATGAGCCACACAGAGAGAGAT 188
QY	181	CTGGGTGGCCCTGCGAGGTGATGCCAGTGTGCGGGCCACTCTGATCTTACC 240
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QY	241	GTCACAGGAGCTTCAAGTGTGCTGCCCTTCCACAGAGCCGTGGCATCGGGATG 300
Db	249	GTCACAGGAGCTTCAAGTGTGCTGCCCTTCCACAGAGCCGTGGCATCGGGATG 308
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QY	361	GCTAACACTCCGTGGGTGATCCAGTGCAGTGTGATAGTGAATGCGGAGCTTC 420
Db	369	GCTAACACTCCGTGGGTGATCCAGTGCAGTGTGATAGTGAATGCGGAGCTTC 428
QY	421	TCCAGGTGTGTATATGATGATGCTCTGAGGGGTGTGCTCCCATGAGCCAGAGCTTCC 480
Db	429	TCCAGGTGTGTATATGATGATGCTCTGAGGGGTGTGCTCCCATGAGCCAGAGCTTCC 488
QY	481	TGCTGTGAAGACAGAGGTGACATGCTGTGCGAGAGGTGCTTCTGACACTGTTCACACC 540

Db 489 TGCTTGAAAGACAGGGTGCATGCTCTCCGACAGGTGCTTTCGACACTGTTTCACACC 548
OY 541 CGCTGCATCACACCCACGGGACCCACCCCTGGCAAGAGCTCCCTGCCAGAGACT 600
Db 549 CGGTGCATCACACCCACGGGACCCACCCCTGGCAAGAGCTCCCTGCCAGAGACT 608
OY 601 AACAGGGCAGTGGCTTTGTCACAGCTGGTCAATGTTCGAGCAGCAGGTCCCGTCCCT 660
Db 609 AACAGGGCAGTGGCTTTGTCACAGCTGGTCAATGTTCGAGCAGCAGGTCCCGTCCCT 668
OY 661 GATGTTTACCTAGCTGTGTAGCTGGCCAGTGGGAGTATGGTGGTCCCAATGGCCCAAC 720
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Db 789 CAGAGTAAGTGGCTTTCACAGGAGAACGCTACAGGAGCTCTCTCACTAACTGCTGCC 848
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Db 849 CACACAGTGGGGATGTGTAATGTGACATGGAGTGGAGTGGCTGCCA 894

RESULT 14
AL544054 888 bp mRNA linear EST 16-FEB-2001
LOCUS AL544054.L1.NFL006.PL2 Homo sapiens cDNA clone CSOD1004YH24 5

DEFINITION prime, mRNA sequence.
ACCESSION AL544054
VERSION AL544054.1 GI:12876533
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 888)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES
source 1..888
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact: Feng Liang life technologies, Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifestech.com URL: http://fulllength.livnet.com"

BASE COUNT 155 a 269 c 255 g 181 t 28 others
ORIGIN

Query Match 40.8%; Score 854.4; DB 9; Length 888;
Best Local Similarity 96.3%; Pred. No. 2.6e-195;
Matches 854; Conservative 23; Mismatches 9; Indels 1; Gaps 1;
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Db 1 TGAGTGGGTGGCTTAACAGCAGGGCTGTGCTGTAACCGGCTCCAGATGTCAGT 60
OY 86 TTAGCCCTGTGGCTCTGCTGCTGAGACCCGAGAGACAGTACAGCTGTGACCGTCCC 145
Db 61 TTAGCCCTGTGGCTCTGCTGCTGAGACCCGAGAGACAGTACAGCTGTGACCGTCCC 120
OY 146 TTTGTGACAAATGGCCACACACTGAGAGAGCATCTGGGTGGCCCTCCAGATTGATG 205
Db 121 TTTGTGACAAATGGCCACACACTGAGAGAGCATCTGGGTGGCCCTCCAGATTGATG 180
OY 206 CCCAGTGTCTGGCCGACCTCTGATCTTTACCTTTCACAGGACTTTCAGTGTGCTGCC 265
Db 181 CCCAGTGTCTGGCCGACCTCTGATCTTTACCTTTCACAGGACTTTCAGTGTGCTGCC 240
OY 266 CTTTCCAGAGGCTGGGATGGGATGGCATATGCTGCTCCACAGGAGCTTTCAGT 325
Db 241 CTTTCCAGAGGCTGGGATGGGATGGCATATGCTGCTCCACAGGAGCTTTCAGT 300
OY 326 GCAGTGCAGACGGGCGATCTGCTTCCAAAGATCAGTAAACAATCCGTGGTCCATCC 385
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OY 446 GCTCTGGGGGTGCTGCTCCCATGCTCCAGAGCTTCTGCTGTGTAAGACAGGATGCT 505
Db 421 GCTCTGGGGGTGCTGCTCCCATGCTCCAGAGCTTCTGCTGTGTAAGACAGGATGCT 480
OY 506 GTCCGACAGGCTGCTTTCGAGACCTGTTACACCCGCTGATACACCCAGGAGCACC 565
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Db 541 ACCCCCTGGCAAGAGCTCCCTGCGCAGAGACTTAACAGGAGGAGTGTGCTGATGCT 600
OY 626 CGGTATGTGTCCGAGCAGGATCCCGGTGCTGATGTTCTTACTGCTGTGAGCTGC 685
Db 601 CGGTATGTGTCCGAGCAGGATCCCGGTGCTGATGTTCTTACTGCTGTGAGCTGC 660
OY 686 CCAGTGGGAATGATGCTGCTGCTGCCAATGCCAAGCCACCTGCTGCTCCGATCCTGC 745
Db 661 CCAGTGGGAATGATGCTGCTGCTGCCAATGCCAAGCCACCTGCTGCTCCGATCCTGC 720
OY 746 ACTGCTGCCCCCAAGACACTGTGTGATGCTGATCCAGATGAGTGCCTCCAGAGAGA 805
Db 721 ACTGCTGCCCCCAAGACACTGTGTGATGCTGATCCAGATGAGTGCCTCCAGAGAGA 780
OY 806 AGCTACACAGGACCTCTCTACTAAGCTCTGCGCAGACAGT-GGGCAGTGTGAATGT 864
Db 781 AGCTACACAGGACCTCTCTACTAAGCTCTGCGCAGACAGTGTGAATGT 840
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RESULT 15
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5', mRNA sequence.
ACCESSION BM468251
VERSION BM468251.1 GI:18517293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 991)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NIH-MGC http://mgi.mcl.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strassberg, Ph.D.
Email: c9abps-r@mail.nih.gov
Tissue Procurement: AFCC/DCMD/MP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12332 row: h column: 17
High quality sequence stop: 670.
Location/Qualifiers
1. 991

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Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 170 a 325 c 295 g 201 t
ORIGIN

Query Match 40.5%; Score 849; DB 13; Length 991;
Best Local Similarity 96.1%; Pred. No. 5.3e-194;
Matches 904; Conservative 0; Mismatches 30; Indels 7; Gaps 3;

QY 1 CGCAGCAGACCATGTTGACCTGTGTAGCTGGGTGACCTTAAACAGCAGGGCTGTGGCT 60
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QY 61 GGAACGGGGTCCCATGTTGCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 120
DB 73 GGAACGGGGTCCCATGTTGCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 132
QY 121 GCCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 133 GCCAGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
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QY 361 GGTAACTACTCGTGGGTGCCATTCAGTGCCTGATAGTCAATGCAATGCCGACTTC 420
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QY 840 GCACACAGTGGGGG---ATGTGAATGTGACATGAGGTGAGCGGCCACAGATGGC---TA 893
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DB 913 ACCTGCTGCTCCGGGTACAGTCCGGGGGCTCCCTGGGGGCTGCC 953

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Job time : 2734 secs

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